

Thu Jun 24 08:47:52 2004

epp526106.pep.rapm

Epperson
09/526106 Page 1
Seq ID 2 (Clariv 63)

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OM protein - protein search, using sw model

Run on: June 19, 2004, 19:08:03 ; Search time 184 Seconds
(without alignments)
1395.120 Million cell updates/sec

Title: EPPER526106.PEP
Perfect score: 1345
Sequence: 1 hpetlvxvkdaedqigaryg.....tmdernqiaigaalikhw 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues
Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

1:	/cgn2_6/ptodata/2/paa/US06_COMB.pep.*
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3:	/cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4:	/cgn2_6/ptodata/2/paa/US08_COMB.pep.*
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9:	/cgn2_6/ptodata/2/paa/US085_COMB.pep.*
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11:	/cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12:	/cgn2_6/ptodata/2/paa/US088_COMB.pep.*
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21:	/cgn2_6/ptodata/2/paa/US097A_COMB.pep.*
22:	/cgn2_6/ptodata/2/paa/US097B_COMB.pep.*
23:	/cgn2_6/ptodata/2/paa/US098_COMB.pep.*
24:	/cgn2_6/ptodata/2/paa/US099A_COMB.pep.*
25:	/cgn2_6/ptodata/2/paa/US099B_COMB.pep.*
26:	/cgn2_6/ptodata/2/paa/US100_COMB.pep.*
27:	/cgn2_6/ptodata/2/paa/US101_COMB.pep.*
28:	/cgn2_6/ptodata/2/paa/US102_COMB.pep.*
29:	/cgn2_6/ptodata/2/paa/US103_COMB.pep.*
30:	/cgn2_6/ptodata/2/paa/US104_COMB.pep.*
31:	/cgn2_6/ptodata/2/paa/US106_COMB.pep.*
32:	/cgn2_6/ptodata/2/paa/US107_COMB.pep.*
33:	/cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1330	98.9	263	19	US-09-526-106-2	Sequence 2, Appli
2	1330	98.9	263	22	US-09-764-163A-2	Sequence 2, Appli
3	1330	98.9	263	22	US-09-791-557-90233	Sequence 90233, A
4	1330	98.9	263	31	US-10-668-778-2	Sequence 2, Appli
5	1330	98.9	286	1	PCT-US02-12405-523	Sequence 523, App
6	1330	98.9	286	1	PCT-US99-17440-7	Sequence 7, Appli
7	1330	98.9	286	1	PCT-US99-17440-14	Sequence 14, Appl
8	1330	98.9	286	1	PCT-US99-17440-21	Sequence 21, Appli
9	1330	98.9	286	15	US-09-129-611-7	Sequence 7, Appli
10	1330	98.9	286	15	US-09-129-611-14	Sequence 14, Appli
11	1330	98.9	286	15	US-09-129-611-21	Sequence 21, Appli
12	1330	98.9	286	18	US-09-490-070-265	Sequence 265, App
13	1330	98.9	286	18	US-09-490-070-362	Sequence 362, App
14	1330	98.9	286	18	US-09-490-070A-265	Sequence 265, App
15	1330	98.9	286	18	US-09-490-070A-362	Sequence 362, App
16	1330	98.9	286	18	US-09-490-153-265	Sequence 265, App
17	1330	98.9	286	18	US-09-490-153-362	Sequence 362, App
18	1330	98.9	286	19	US-09-529-967-10	Sequence 10, Appli
19	1330	98.9	286	23	US-09-837-306-354	Sequence 354, App
20	1330	98.9	286	25	US-09-980-585-4	Sequence 4, Appli
21	1330	98.9	286	25	US-09-980-585A-4	Sequence 4, Appli
22	1330	98.9	286	26	US-10-045-674-523	Sequence 523, App
23	1330	98.9	286	27	US-10-191-966-7	Sequence 7, Appli
24	1330	98.9	286	27	US-10-191-966-14	Sequence 14, Appli
25	1330	98.9	286	27	US-10-191-966-21	Sequence 21, Appli
26	1330	98.9	286	30	US-10-405-027-3366	Sequence 3366, App
27	1330	98.9	286	30	US-10-405-027-3369	Sequence 3369, App
28	1330	98.9	286	30	US-10-405-027-4786	Sequence 4786, App
29	1330	98.9	290	1	PCT-US01-01239-1215	Sequence 1215, App
30	1330	98.9	290	12	US-09-764-902-1215	Sequence 11955, A
31	1330	98.9	290	22	US-09-764-905-11955	Sequence 11955, A
32	1330	98.9	290	22	US-09-764-905-11955	Sequence 11955, A
33	1330	98.9	290	26	US-10-092-339-11955	Sequence 285, App
34	1330	98.9	299	18	US-09-490-070-285	Sequence 285, App
35	1330	98.9	299	18	US-09-490-070-298	Sequence 298, App
36	1330	98.9	299	18	US-09-490-070-300	Sequence 300, App
37	1330	98.9	299	18	US-09-490-070A-285	Sequence 285, App
38	1330	98.9	299	18	US-09-490-070A-298	Sequence 298, App
39	1330	98.9	299	18	US-09-490-070A-300	Sequence 300, App
40	1330	98.9	299	18	US-09-490-153-285	Sequence 285, App
41	1330	98.9	299	18	US-09-490-153-298	Sequence 298, App
42	1330	98.9	299	18	US-09-490-153-300	Sequence 300, App
43	1330	98.9	2307	1	PCT-US99-17440-2	Sequence 2, Appli
44	1330	98.9	2307	1	PCT-US99-17440-9	Sequence 9, Appli
45	1330	98.9	2307	1	PCT-US99-17440-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-09-526-106-2
; Sequence 2, Application US/09526106
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Kalobios, Inc.
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-000700US
; CURRENT APPLICATION NUMBER: US/09/526,106
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124,339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135,926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli

FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-09-526-106-2

Query Match 98.9%; Score 1330; DB 19; Length 263;
Best Local Similarity 98.9%; Pred. No. 5.2e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGARVGYIELDINSGETLESFRSEERPFPMSTFVLLCGAVLSRID 60
DB 1 HPEITLVKKAEDQAGARVGYIELDINSGETLESFRSEERPFPMSTFVLLCGAVLSRID 60
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
QY 121 KELTAFIHNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTLRKLLTGBLLTLASRQ 180
DB 121 KELTAFIHNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTLRKLLTGBLLTLASRQ 180
QY 181 QLIIMMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDGKPSRIIVITYTG 240
DB 181 QLIIMMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDGKPSRIIVITYTG 240
QY 241 SQATMDERNROIATIGASLIKH 263
DB 241 SQATMDERNROIATIGASLIKH 263

RESULT 2
US-09-764-163A-2

Sequence 2, Application US/09764163A
GENERAL INFORMATION:
APPLICANT: Balint, Robert F.
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Circularly Permuted, Interaction-Activated Proteins
FILE REFERENCE: 021167-000710US
CURRENT APPLICATION NUMBER: US/09/764.163A
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: US 09/526,106
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-09-764-163A-2

Query Match 98.9%; Score 1330; DB 22; Length 263;
Best Local Similarity 98.9%; Pred. No. 5.2e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGARVGYIELDINSGETLESFRSEERPFPMSTFVLLCGAVLSRID 60
DB 1 HPEITLVKKAEDQAGARVGYIELDINSGETLESFRSEERPFPMSTFVLLCGAVLSRID 60
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
QY 121 KELTAFIHNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTLRKLLTGBLLTLASRQ 180
DB 121 KELTAFIHNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTLRKLLTGBLLTLASRQ 180
QY 181 QLIIMMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDGKPSRIIVITYTG 240
DB 181 QLIIMMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDGKPSRIIVITYTG 240

QY 241 SQATMDERNROIATIGASLIKH 263
DB 241 SQATMDERNROIATIGASLIKH 263

RESULT 3
US-09-791-537-90233

Sequence 90233, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMEB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90233
LENGTH: 263
TYPE: PRT
ORGANISM: pdb 1BTL
US-09-791-537-90233

Query Match 98.9%; Score 1330; DB 22; Length 263;
Best Local Similarity 98.9%; Pred. No. 5.2e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGARVGYIELDINSGETLESFRSEERPFPMSTFVLLCGAVLSRID 60
DB 1 HPEITLVKKAEDQAGARVGYIELDINSGETLESFRSEERPFPMSTFVLLCGAVLSRID 60
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
QY 121 KELTAFIHNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTLRKLLTGBLLTLASRQ 180
DB 121 KELTAFIHNMGDHYTRLDREPELNEALPNDERDTTVPVAMATTLRKLLTGBLLTLASRQ 180
QY 181 QLIIMMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDGKPSRIIVITYTG 240
DB 181 QLIIMMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDGKPSRIIVITYTG 240
QY 241 SQATMDERNROIATIGASLIKH 263
DB 241 SQATMDERNROIATIGASLIKH 263

RESULT 4
US-10-668-778-2

Sequence 2, Application US/10668778
GENERAL INFORMATION:
APPLICANT: Balint, Robert F.
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668.778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 98.9%; Score 1330; DB 31; Length 263;
Best Local Similarity 98.9%; Pred. No. 5.2e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQDQGVGVYIELDNSGEILSRSEERFPMMSTFKVLLCGAVLSRID 60
DB 1 HPELVKVDADQDQGVGVYIELDNSGEILSRSEERFPMMSTFKVLLCGAVLSRID 60
QY 61 AGQEQGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
DB 61 AGQEQGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
QY 121 KETLAFLNMGDHTVRLDRWEPELNEAIPNDRDTPVAMATTIRKLLTGELLTASRQ 180
DB 121 KETLAFLNMGDHTVRLDRWEPELNEAIPNDRDTPVAMATTIRKLLTGELLTASRQ 180
QY 181 QLIDMNEADKVAQPLIRSAIPAGMFIADKSGAGERSGRIIAALGPDGKPSRIIVITYTG 240
DB 181 QLIDMNEADKVAQPLIRSAIPAGMFIADKSGAGERSGRIIAALGPDGKPSRIIVITYTG 240
QY 241 SQATMDERNROIAETIGASLIKHW 263
DB 241 SQATMDERNROIAETIGASLIKHW 263

RESULT 5

PCT-US02-12405-523
Sequence 523, Application PC/TUS0212405
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: KOOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: PCT/US02/12405
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCRESS
OTHER INFORMATION: protein sequence
PCT-US02-12405-523

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQDQGVGVYIELDNSGEILSRSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQDQGVGVYIELDNSGEILSRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120

DB 84 AGQEQGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KETLAFLNMGDHTVRLDRWEPELNEAIPNDRDTPVAMATTIRKLLTGELLTASRQ 180
DB 144 KETLAFLNMGDHTVRLDRWEPELNEAIPNDRDTPVAMATTIRKLLTGELLTASRQ 203
QY 181 QLIDMNEADKVAQPLIRSAIPAGMFIADKSGAGERSGRIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDMNEADKVAQPLIRSAIPAGMFIADKSGAGERSGRIIAALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNROIAETIGASLIKHW 263
DB 264 SQATMDERNROIAETIGASLIKHW 286

RESULT 6

PCT-US99-17440-7
Sequence 7, Application PC/TUS9917440
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: PCT/US99/17440
CURRENT FILING DATE: 1999-08-02
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
PCT-US99-17440-7

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQDQGVGVYIELDNSGEILSRSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQDQGVGVYIELDNSGEILSRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
DB 84 AGQEQGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KETLAFLNMGDHTVRLDRWEPELNEAIPNDRDTPVAMATTIRKLLTGELLTASRQ 180
DB 144 KETLAFLNMGDHTVRLDRWEPELNEAIPNDRDTPVAMATTIRKLLTGELLTASRQ 203
QY 181 QLIDMNEADKVAQPLIRSAIPAGMFIADKSGAGERSGRIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDMNEADKVAQPLIRSAIPAGMFIADKSGAGERSGRIIAALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNROIAETIGASLIKHW 263
DB 264 SQATMDERNROIAETIGASLIKHW 286

RESULT 7

PCT-US99-17440-14
Sequence 14, Application PC/TUS9917440
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: PCT/US99/17440
CURRENT FILING DATE: 1999-08-02
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
PCT-US99-17440-14

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDOLGARVGYIELDLSGELLESFRSEPRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADQDOLGARVGYIELDLSGKILLESFRSEPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSQNDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAAILTTIGSP 120
DB 84 AGGOLGRRIHYSQNDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAAILTTIGSP 143
QY 121 KETLAFHNMGDHYTRLDRWPEELNEALPNDERDTTPVAMATTLRKLLTGBLLTLASRQ 180
DB 144 KETLAFHNMGDHYTRLDRWPEELNEALPNDERDTTPVAMATTLRKLLTGBLLTLASRQ 203
QY 181 QLIDMWEADKYAGPLRLSALPAGWFIADKSGAGRGSGIITAAIGDGPSPRIIVYITGG 240
DB 204 QLIDMWEADKYAGPLRLSALPAGWFIADKSGAGRGSGIITAAIGDGPSPRIIVYITGG 263
QY 241 SOATMDERNROIABIGASLIKH 263
DB 264 SOATMDERNROIABIGASLIKH 286

RESULT 8

PCT-US99-17440-21
Sequence 21, Application PC/TUS9917440
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: PCT/US99/17440
CURRENT FILING DATE: 1999-08-02
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
PCT-US99-17440-21

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDOLGARVGYIELDLSGELLESFRSEPRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADQDOLGARVGYIELDLSGKILLESFRSEPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSQNDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAAILTTIGSP 120
DB 84 AGGOLGRRIHYSQNDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAAILTTIGSP 143
QY 121 KETLAFHNMGDHYTRLDRWPEELNEALPNDERDTTPVAMATTLRKLLTGBLLTLASRQ 180

DB 144 KETLAFHNMGDHYTRLDRWPEELNEALPNDERDTTPVAMATTLRKLLTGBLLTLASRQ 203
QY 181 QLIDMWEADKYAGPLRLSALPAGWFIADKSGAGRGSGIITAAIGDGPSPRIIVYITGG 240
DB 204 QLIDMWEADKYAGPLRLSALPAGWFIADKSGAGRGSGIITAAIGDGPSPRIIVYITGG 263
QY 241 SOATMDERNROIABIGASLIKH 263
DB 264 SOATMDERNROIABIGASLIKH 286

RESULT 9

US-09-129-611-7
Sequence 7, Application US/09129611A
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/129,611A
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-129-611-7

Query Match 98.9%; Score 1330; DB 15; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDOLGARVGYIELDLSGELLESFRSEPRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADQDOLGARVGYIELDLSGKILLESFRSEPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSQNDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAAILTTIGSP 120
DB 84 AGGOLGRRIHYSQNDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAAILTTIGSP 143
QY 121 KETLAFHNMGDHYTRLDRWPEELNEALPNDERDTTPVAMATTLRKLLTGBLLTLASRQ 180
DB 144 KETLAFHNMGDHYTRLDRWPEELNEALPNDERDTTPVAMATTLRKLLTGBLLTLASRQ 203
QY 181 QLIDMWEADKYAGPLRLSALPAGWFIADKSGAGRGSGIITAAIGDGPSPRIIVYITGG 240
DB 204 QLIDMWEADKYAGPLRLSALPAGWFIADKSGAGRGSGIITAAIGDGPSPRIIVYITGG 263
QY 241 SOATMDERNROIABIGASLIKH 263
DB 264 SOATMDERNROIABIGASLIKH 286

RESULT 10

US-09-129-611-14
Sequence 14, Application US/09129611A
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/129,611A
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-129-611-14

Query Match 98.9%; Score 1330; DB 15; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVYIELDINSGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQOLGARVYIELDINSGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEQUGRIHYSONDIVESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
DB 84 AGGEQUGRIHYSONDIVESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
QY 121 KETLTAFLHNMGDHVTLRDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 180
DB 144 KETLTAFLHNMGDHVTLRDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLRLSALPAGWFTADKSGAGERSRGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAQPLRLSALPAGWFTADKSGAGERSRGIIAALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNQIAEIGASLIKHW 263
DB 264 SQATMDERNQIAEIGASLIKHW 266

RESULT 11
US-09-129-611-21
Sequence 21, Application US/09129611A
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/129, 611A
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 09/129, 611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-129-611-21

Query Match 98.9%; Score 1330; DB 15; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVYIELDINSGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQOLGARVYIELDINSGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEQUGRIHYSONDIVESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
DB 84 AGGEQUGRIHYSONDIVESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
QY 121 KETLTAFLHNMGDHVTLRDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 180
DB 144 KETLTAFLHNMGDHVTLRDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLRLSALPAGWFTADKSGAGERSRGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAQPLRLSALPAGWFTADKSGAGERSRGIIAALGPDGKPSRIIVITYTG 263

QY 241 SQATMDERNQIAEIGASLIKHW 263
DB 264 SQATMDERNQIAEIGASLIKHW 286

RESULT 12
US-09-490-070-265
Sequence 265, Application US/09490070
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ileg, Vic
Ge, Laming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490, 070
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/025,769
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070-265

Query Match 98.9%; Score 1330; DB 18; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVYIELDINSGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQOLGARVYIELDINSGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEQUGRIHYSONDIVESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
DB 84 AGGEQUGRIHYSONDIVESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
QY 121 KETLTAFLHNMGDHVTLRDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 180
DB 144 KETLTAFLHNMGDHVTLRDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLRLSALPAGWFTADKSGAGERSRGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAQPLRLSALPAGWFTADKSGAGERSRGIIAALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNQIAEIGASLIKHW 263

Db 264 SQAATMDERNROJAEIGASLIIKHW 286

RESULT 13

US-09-490-070-362

; Sequence 362, Application US/09490070

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESSES:

; ADDRESSSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070

; FILING DATE: 24-Jan-2000

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 09/025,769

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 362:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-070-362

Query Match 98.9%; Score 1330; DB 18; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 HPEITLVKVDADQIGARVGYIELDINSGEIIIESRSEERFPFMSSTFKYLICGAVLSRID 60
24 HPEITLVKVDADQIGARVGYIELDINSGEIIIESRSEERFPFMSSTFKYLICGAVLSRID 83
61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGKTVBELCSAATMSDNTAANLLTTTIGSP 120
84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGKTVBELCSAATMSDNTAANLLTTTIGSP 143
121 KELTAFILNMGDHVTLRDWEPELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 180
144 KELTAFILNMGDHVTLRDWEPELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203
181 QIIDMWEADKVAQPLIRSLPAGWFIADKSGAGERGSRGIIALGPDPGKPSRIIVVITYTG 240
204 QIIDMWEADKVAQPLIRSLPAGWFIADKSGAGERGSRGIIALGPDPGKPSRIIVVITYTG 263
241 SQAATMDERNROJAEIGASLIIKHW 263
264 SQAATMDERNROJAEIGASLIIKHW 286

RESULT 14

US-09-490-070A-265

; Sequence 265, Application US/09490070A

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESSES:

; ADDRESSSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

; STREET: 1666 K Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070A

; FILING DATE: 24-Jan-2000

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Colin G. Sandercock, Esq.

; REGISTRATION NUMBER: 31,298

; REFERENCE/DOCKET NUMBER: 37629-0005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 912-2000

; TELEFAX: (202) 912-2020

; INFORMATION FOR SEQ ID NO: 265:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 98.9%; Score 1330; DB 18; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 HPEITLVKVDADQIGARVGYIELDINSGEIIIESRSEERFPFMSSTFKYLICGAVLSRID 60
24 HPEITLVKVDADQIGARVGYIELDINSGEIIIESRSEERFPFMSSTFKYLICGAVLSRID 83
61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGKTVBELCSAATMSDNTAANLLTTTIGSP 120
84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGKTVBELCSAATMSDNTAANLLTTTIGSP 143
121 KELTAFILNMGDHVTLRDWEPELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 180
144 KELTAFILNMGDHVTLRDWEPELNEAIPNDRDITTPVAMATTIRKLLTGELITLASRQ 203
181 QIIDMWEADKVAQPLIRSLPAGWFIADKSGAGERGSRGIIALGPDPGKPSRIIVVITYTG 240
204 QIIDMWEADKVAQPLIRSLPAGWFIADKSGAGERGSRGIIALGPDPGKPSRIIVVITYTG 263
241 SQAATMDERNROJAEIGASLIIKHW 263
264 SQAATMDERNROJAEIGASLIIKHW 286

Search completed: June 18, 2004, 19:13:52
Job time : 185 secs

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RESULT 15
US-09-490-070A-362
; Sequence 362, Application US/09490070A
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;   White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match          98.9%; Score 1330; DB 18; Length 286;
Best Local Similarity 98.9%; Pred. No. 66-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQIGARVGYIELDINSGEILLESFRSEERFPWMTFKYLLCGAVLSRID 60
Db- HPEITLVKVDADQIGARVGYIELDINSGEILLESFRSEERFPWMTFKYLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLVESPTVEKHLTDGNTVRELCSAALTMSDNTANILITTTIGSP 120
Db AGQEQIGRIHYSQNDLVESPTVEKHLTDGNTVRELCSAALTMSDNTANILITTTIGSP 143
QY 121 KELTAFLEHMGDHTVRLDRMBPELNEAIPNDRDFTTPVAMATTLRKLLTGELTLASRQ 180
Db KELTAFLEHMGDHTVRLDRMBPELNEAIPNDRDFTTPVAMATTLRKLLTGELTLASRQ 203
QY 144 KELTAFLEHMGDHTVRLDRMBPELNEAIPNDRDFTTPVAMATTLRKLLTGELTLASRQ 203
Db 144 KELTAFLEHMGDHTVRLDRMBPELNEAIPNDRDFTTPVAMATTLRKLLTGELTLASRQ 203
QY 181 QILDMWEADKVAGPLIRSLPAGWFIADKSGAGERSRGIITAGLPDGPSPRIIVITYTTG 240
Db 181 QILDMWEADKVAGPLIRSLPAGWFIADKSGAGERSRGIITAGLPDGPSPRIIVITYTTG 240
QY 204 QILDMWEADKVAGPLIRSLPAGWFIADKSGAGERSRGIITAGLPDGPSPRIIVITYTTG 263
Db 204 QILDMWEADKVAGPLIRSLPAGWFIADKSGAGERSRGIITAGLPDGPSPRIIVITYTTG 263
QY 241 SQATMDERNROIAETGASLIKHW 263
Db 241 SQATMDERNROIAETGASLIKHW 263
QY 264 SQATMDERNROIAETGASLIKHW 286
Db 264 SQATMDERNROIAETGASLIKHW 286

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:30:18 ; Search time 18 Seconds

(without alignments)
760.803 Million cell updates/sec

Title: EPPER526106.PEP
Perfect score: 1345
Sequence: 1 hpctlvkvkaedqlgaryg.....tmdermqaeigsalikhw 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1325	98.5	286	1 BLAT_ECOLI	P00810 <i>Escherichia</i>
2	942	70.0	286	1 BLAI_ECOLI	P14557 <i>Escherichia</i>
3	940	69.9	286	1 BLI3_KLEPN	O95424 <i>Klebsiella</i>
4	937	69.7	286	1 BLA8_ECOLI	O08337 <i>Escherichia</i>
5	936	69.6	286	1 BLA2_ECOLI	P14558 <i>Escherichia</i>
6	935	69.5	286	1 BLA2_ECOLI	O95424 <i>Escherichia</i>
7	933	69.4	286	1 BLA3_KLEPN	P30896 <i>Klebsiella</i>
8	932	69.3	286	1 BLA5_KLEPN	P37320 <i>Klebsiella</i>
9	929	69.1	265	1 BLA4_KLEPN	P37323 <i>Klebsiella</i>
10	905	67.3	279	1 BLA6_KLEPN	P05192 <i>Klebsiella</i>
11	879	65.4	260	1 BLA6_KLEPN	P96348 <i>Klebsiella</i>
12	874	65.0	286	1 BLAI_ENTCL	P18251 <i>Enterobacte</i>
13	672	50.0	298	1 BLAI_PROMI	P30897 <i>proteus mir</i>
14	573	42.6	304	1 BLAI_AERYH	O44056 <i>aeromonas h</i>
15	539.5	40.1	288	1 BLI3_PSEAE	P37322 <i>pseudomonas</i>
16	539.5	40.1	288	1 BLI4_PSEAE	P16897 <i>pseudomonas</i>
17	536.5	39.9	288	1 BLI6_PSEAE	P16897 <i>pseudomonas</i>
18	535.5	39.8	288	1 BLI1_PSEAE	P16897 <i>pseudomonas</i>
19	516.5	38.4	290	1 BLI2_KLEOX	O03170 <i>pseudomonas</i>
20	513.5	38.2	291	1 BLI1_KLEOX	P22391 <i>Klebsiella</i>
21	512.5	38.1	293	1 BLI1_KLEOX	P22391 <i>Klebsiella</i>
22	505.5	37.6	302	1 BLI1_KLEOX	P22391 <i>Klebsiella</i>
23	498.5	37.1	288	1 BLI1_KLEOX	O06316 <i>nocardia la</i>
24	496.5	36.9	294	1 BLI1_KLEOX	O51355 <i>pseudomonas</i>
25	494.5	36.8	306	1 BLI1_KLEOX	O01166 <i>yersinia en</i>
26	490	36.4	305	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
27	489.5	36.4	305	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
28	487	36.2	291	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
29	486.5	36.2	267	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
30	483.5	35.9	306	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
31	483	35.9	306	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
32	482.5	35.9	306	1 BLI1_KLEOX	P35392 <i>streptomyce</i>
33	477	35.5	291	1 BLI1_KLEOX	P35392 <i>streptomyce</i>

34	476	35.4	303	1 BLA2_XANMA	P96465 <i>xanthomonas</i>
35	474	35.2	291	1 BLI3_SALTY	O33807 <i>salmonella</i>
36	471.5	35.1	294	1 BLA2_CITDI	P22390 <i>citrobacter</i>
37	471	35.0	291	1 BLI5_SALTY	O65975 <i>salmonella</i>
38	467.5	34.8	309	1 BLA2_SALTY	O45726 <i>bacillus th</i>
39	467	34.7	291	1 BLI6_SALTY	O65976 <i>salmonella</i>
40	466.5	34.7	311	1 BLA2_SALTY	O65976 <i>salmonella</i>
41	462	34.3	325	1 BLA1_STRCI	O06650 <i>streptomyce</i>
42	459.5	34.2	305	1 BLA2_STRCI	O03680 <i>streptomyce</i>
43	458.5	34.1	294	1 BLA1_MYCFO	P35393 <i>streptomyce</i>
44	456	33.9	306	1 BLA2_BACCE	O59517 <i>mycobacteri</i>
45	455.5	33.9	306	1 BLA1_BACMY	P00809 <i>bacillus ce</i>
					P28018 <i>bacillus my</i>

ALIGNMENTS

RESULT 1
BLAT_ECOLI
ID BLAT_ECOLI STANDARD; PRT; 286 AA.
AC P00810; Q47313;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3)
DE (TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6)
DE (IRT-4) (Pencilillinase).
GN (BLA OR HCM.216) AND BLAT-3 AND BLAT-4 AND BLAT-5 AND BLAT-6.
OS *Escherichia coli*, and
OS *Salmonella typhi*.
OG Plasmid R1 (R7268), Plasmid IncFII R100, Plasmid R6K, Plasmid pUD16,
OG Plasmid pCFP04, Plasmid pCFP14, and Plasmid pHCM1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Escherichia*.
OX NCBI_Taxid=562, 601;
RN [1]
RP SEQUENCE FROM N.A. (TEM-1).
RC SPECIES=E.coli; PLASMID=R1 (R7268); TRANSPOSON=Tn3;
RX MEDLINE=79012484; PubMed=358200;
RA Sutcliffe J.G.;
RT "Nucleotide sequence of the ampicillin resistance gene of *Escherichia coli* plasmid pBR322.";
RT Proc. Natl. Acad. Sci. U.S.A. 75:3737-3741 (1978).
RN [2]
RP SEQUENCE FROM N.A. (TEM-1).
RC SPECIES=E.coli; PLASMID=R1 (R7268); TRANSPOSON=Tn3;
RX MEDLINE=80002802; PubMed=383387;
RA Sutcliffe J.G.;
RT "Complete nucleotide sequence of the *Escherichia coli* plasmid pBR322.";
RT Cold Spring Harb. Symp. Quant. Biol. 43:77-90 (1979).
RN [3]
RP SEQUENCE FROM N.A. (TEM-1).
RC PLASMID=IncFII R100;
RX MEDLINE=86319522; PubMed=3019092;
RA Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;
RT "DNA replication of the resistance plasmid R100 and its control.";
RT Adv. Biophys. 21:115-133 (1986).
RN [4]
RP SEQUENCE OF 24-286 (TEM-2).
RC SPECIES=E.coli; PLASMID=R6K; TRANSPOSON=Tn1;
RX MEDLINE=79012483; PubMed=358199;
RA Ambler R.P., Scott G.K.;
RT "Partial amino acid sequence of penicillinase coded by *Escherichia coli* plasmid R6K.";
RT Proc. Natl. Acad. Sci. U.S.A. 75:3732-3736 (1978).
RN [5]
RP SEQUENCE FROM N.A. (TEM-3).
RA Soukaiif W., Goussard S., Courvalin P.;
RT "The TEM-3 beta-lactamase, which hydrolyzes broad-spectrum cephalosporins, is derived from the TEM-2 penicillinase by two amino acid substitutions.";
RT FEBS Microbiol. Lett. 56:343-348 (1988).

[6] RP SEQUENCE FROM N.A. (TEM-3).
 RC PLASMID=PCF04;
 RX MEDLINE=93062798; PubMed=1331747;
 RA Mahlat C., Lourencao-Vital J., Goussard S., Courvalin P.;
 RT "A new example of physical linkage between Tnl and Tn21: the
 RT antibiotic multiple-resistance region of plasmid pCF04 encoding
 RT extended-spectrum beta-lactamase TEM-3.";
 RL Mol. Genet. 235:113-121 (1992).
 RN [7]
 RP SEQUENCE FROM N.A. (TEM-4 AND TEM-5).
 RC STRAIN=CB86134; PLASMID=pUD16; and pCF04;
 RX MEDLINE=89378760; PubMed=2550326;
 RA Sougakoff W., Petit A., Goussard S., Sirost D., Bure A., Courvalin P.;
 RT "Characterization of the plasmid genes blaT-4 and blaT-5 which encode
 RT the broad-spectrum beta-lactamase TEM-4 and TEM-5 in
 RT enterobacteriaceae.";
 RL Gene 78:339-348 (1989).
 RN [8]
 RP SEQUENCE FROM N.A. (TEM-6).
 RC STRAIN=HB251;
 RX MEDLINE=92166702; PubMed=165171;
 RA Goussard S., Sougakoff W., Mahlat C., Bauernfeind A., Courvalin P.;
 RT "An ISI-like element is responsible for high-level synthesis of
 RT extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae.";
 RL J. Gen. Microbiol. 137:2681-2687 (1991).
 RN [9]
 RP SEQUENCE FROM N.A. (TEM-8; TEM-16 AND TEM-24).
 RX MEDLINE=93037315; PubMed=1416873;
 RA Chahal C., Poupart M.C., Sirost D., Labia R., Sirost J., Cluzel R.;
 RT "Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase
 RT genes";
 RL Antimicrob. Agents Chemother. 36:1817-1820 (1992).
 RN [10]
 RP SEQUENCE OF 24-286 (IRT-4).
 RC STRAIN=PEV;
 RX MEDLINE=94333751; PubMed=8056282;
 RA Brun T., Peduzzi J., Canica M.M., Paul G., Nevot P., Barthelemy M.,
 RA Labia R.;
 RT "Characterization and amino acid sequence of IRT-4, a novel TEM-type
 RT enzyme with a decreased susceptibility to beta-lactamase
 RT inhibitors";
 RL FEMS Microbiol. Lett. 120:111-117 (1994).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. typhi; STRAIN=CT18; PLASMID=pHCM1;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Relwell I., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagals K.,
 RA Krogh A., Larsen T.S., Leather S., Moutle S., O'Garra P., Parry C.,
 RA Quail M.A., Rutherford K., Simmonds W., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852 (2001).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF TEM-1.
 RX MEDLINE=92183921; PubMed=1544485;
 RA Telach C., Lentant F., Masson J.-M., Samama J.-P.;
 RT "beta-lactamase TEM1 of *E. coli*. Crystal structure determination at
 RT 2.5-A resolution.";
 RL FEBS Lett. 299:135-142 (1992).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF TEM-1.
 RX MEDLINE=93361453; PubMed=8356032;
 RA Telach C., Mouney L., Masson J.-M., Samama J.-P.;
 RT "Crystal structure of *Escherichia coli* TEM1 beta-lactamase at 1.8-A
 RT resolution.";
 RL Proteins 16:364-383 (1993).
 RN [14]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF TEM-1 COMPLEXED WITH BLIP.
 RX MEDLINE=96186252; PubMed=8605632;
 RA Strynadka N.C.J., Jensen S.E., Alzari P.M., James M.N.G.;
 RT "A potent new mode of beta-lactamase inhibition revealed by the 1.7 A
 RT X-ray crystallographic structure of the TEM-1-BLIP complex.";
 RL Nat. Struct. Biol. 3:290-297 (1996).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF TEM-1.
 RX MEDLINE=98151145; PubMed=9485412;
 RA Mayevraud L., Pratt R.F., Samama J.-P.;
 RT "Crystal structure of an acylation transition-state analog of the
 RT TEM-1 beta-lactamase. Mechanistic implications for class A beta-
 RT lactamases.";
 RL Biochemistry 37:2622-2628 (1998).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF TEM-1.
 RX MEDLINE=99352177; PubMed=10423234;
 RA Swaren P., Golemi D., Cabanots S., Bulchev A., Mayevraud L.,
 RA Mobashery S., Samama J.-P.;
 RT "X-ray structure of the Asn276Asp variant of the *Escherichia coli*
 RT TEM-1 beta-lactamase: direct observation of electrostatic modulation
 RT in resistance to inactivation by clavulanic acid.";
 RL Biochemistry 38:9570-9576 (1999).
 RN [17]
 RP BIOCHEMISTRY: TEM-TYPE ARE THE MOST PREVALENT BETA-LACTAMASES IN
 CC ENTEROBACTERIA; THEY HYDROLYZE THE BETA-LACTAM BOND IN SUSCEPTIBLE
 CC BETA-LACTAM ANTIBIOTICS, THUS CONFERRING RESISTANCE TO PENICILLINS
 CC AND CEPHALOSPORINS. TEM-3 AND TEM-4 ARE CAPABLE OF HYDROLYZING
 CC CEFOTAXIME AND CEFCAZIDIME. TEM-5 IS CAPABLE OF HYDROLYZING
 CC AZTREONAM. TEM-8/CAZ-2, TEM-16/CAZ-7 AND TEM-24/CAZ-6 ARE MARKEDLY
 CC ACTIVE AGAINST CEFCAZIDIME. IRT-4 SHOWS RESISTANCE TO BETA-
 CC LACTAMASE INHIBITORS.
 CC [18]
 RP CATALYTIC ACTIVITY: A beta-lactam + H(2O) = a substituted beta-
 CC amino acid.
 CC [19]
 RP BIOTECHNOLOGY: THIS PROTEIN IS USED AS A MARKER IN MANY COMMONLY
 CC USED CLONING VECTORS, SUCH AS pBR322 AND THE pUC SERIES.
 CC [20]
 RP MISCELLANEOUS: THE BETA-LACTAMASE PRESENT ON pBR322 WAS CLONED
 CC FROM PLASMID RI (R7268).
 CC [21]
 RP SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
 CC [22]
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 CC [23]
 RP EMBL: J01749; AA859737.1; -
 DR EMBL: V00613; CAA23886.1; -
 DR EMBL: X64523; CAA45828.1; -
 DR EMBL: X57972; CAA41038.1; -
 DR EMBL: X65252; CAA46344.1; -
 DR EMBL: X65253; CAA46345.1; -
 DR EMBL: X65254; CAA46346.1; -
 DR EMBL: X85284; AAB64366.1; -
 DR EMBL: U66885; AAC48875.1; -
 DR EMBL: AL513383; CAD09800.1; -
 DR PIR: A93821; PNECP.
 DR PIR: S10113; S30113.
 DR PDB: 1BTL; 26-JAN-95.
 DR PDB: 1TEM; 15-MAY-97.
 DR PDB: 1XPB; 01-APR-97.
 DR PDB: 1AXB; 18-NOV-98.
 DR PDB: 1CKJ; 18-AUG-99.
 DR PDB: 1PMS; 02-SEP-99.
 DR PDB: 1ERM; 20-DEC-00.
 DR PDB: 1ERO; 20-DEC-00.
 DR PDB: 1ESU; 03-MAY-00.
 DR PDB: 1FOG; 01-NOV-00.
 DR PDB: 1TMD; 18-DEC-02.
 DR PDB: 1UTG; 17-OCT-01.

Query Match 98.5%; Score 1325; DB 1; Length 286;
 Best Local Similarity 98.1%; Pred. No. 6.6e-96;
 Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPELVKVAEDQGVGIIELDINSGETLSEFSEERPPMMSTFEVLLCGAVLRID 60
 DB 24 HPELVKVAEDQGVGIIELDINSGETLSEFSEERPPMMSTFEVLLCGAVLRID 83
 QY 61 AGGQGLRRTHYSQNDIVSESPVTEKHLTDGTVRELCSAATMSDNTAANLLTTTIGP 120
 DB 84 AGGQGLRRTHYSQNDIVSESPVTEKHLTDGTVRELCSAATMSDNTAANLLTTTIGP 143
 QY 121 KETLAFIANNGDHVTIRLDREPELNEAIPNDERPTTPVAMATTIRKLLTCELLTASRQ 180
 DB 144 KETLAFIANNGDHVTIRLDREPELNEAIPNDERPTTPVAMATTIRKLLTCELLTASRQ 203
 QY 181 QLDWMEDADVAGPGLRSALPAGWFIADKSGAGERSRGITIAALGPGKPSRIVITYTG 240
 DB 204 QLDWMEDADVAGPGLRSALPAGWFIADKSGAGERSRGITIAALGPGKPSRIVITYTG 263
 QY 241 SQATMDERNQIAEIGASLTKHW 263
 DB 264 SQATMDERNQIAEIGASLTKHW 286

RESULT 2
 BLA1_ECOLI STANDARD; PRT; 286 AA.
 ID BLA1_ECOLI STANDARD; PRT; 286 AA.
 AC P14557; 007941; P23982;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-lactamase SHV-1 precursor (EC 3.5.2.6) (PIT-2).
 GN BIA OR SHV1.
 OS Escherichia coli, and
 OS Klebsiella pneumoniae.
 OG Plasmid R974, and plasmid p453.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562, 573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=K.pneumoniae; PLASMID=R974;
 RX MEDLINE=91024126; PubMed=2221867;
 RA Mercier J., Levesque R.C.;
 RT "Cloning of SHV-2, OHIO-1, and OXA-6 beta-lactamases and cloning and
 RL sequencing of SHV-1 beta-lactamase."
 RN Antimicrob. Agents Chemother. 34:1577-1583 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=K.pneumoniae; STRAIN=KPA-1, KPZU-8, and KPZU-13;
 RX MEDLINE=97281235; PubMed=9145849;
 RA Nuesch-Indebien M., Kayser F.H., Hachler H.;
 RT "Survey and molecular genetics of SHV beta-lactamases in
 RN Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and SHV-
 RT 12."
 RN Antimicrob. Agents Chemother. 41:943-949 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=K.pneumoniae; STRAIN=15571;
 RA Rice L.B., Bonafede M., Hujer A.M., Bonomo R.A.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=HB101;
 RA Bradford P.A.;
 RT "Automated thermal cycling is superior to traditional methods for
 RL nucleotide sequencing of blaSHV genes."
 RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RC [5]
 RP SEQUENCE OF 22-286.
 RC SPECIES=E.coli; PLASMID=p453;

RX MEDLINE=88268817; PubMed=3260490;
 RA Barthelemy M., Peduzzi J., Labia R.;
 RT "Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-
 RL lactamase (SHV-1)."
 RN Biochem. J. 251:73-79 (1988).
 RN [6]
 RP SEQUENCE OF 22-128.
 RC SPECIES=E.coli; PLASMID=p453;
 RX MEDLINE=87279638; PubMed=497152;
 RA Barthelemy M., Peduzzi J., Labia R.;
 RT "N-terminal amino acid sequence of PIT-2 beta-lactamase (SHV-1)."
 RN Antimicrob. Chemother. 19:839-841 (1987).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
 RC SPECIES=K.pneumoniae; STRAIN=15571;
 RX MEDLINE=99249781; PubMed=10231522;
 RA Kuzin A.P., Nukaga M., Nukaga Y., Hujer A.M., Bonomo R.A., Knox J.R.;
 RT "Structure of the SHV-1 beta-lactamase."
 RL Biochemistry 38:5720-5727 (1999).
 RL -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. DIFFERS
 CC IN ONLY ONE POSITION FROM SHV-2.
 CC -----
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 CC -----
 DR EMBL; MS9181; AAA26087.1; -;
 DR EMBL; X98098; CA466726.1; -;
 DR EMBL; X98099; CA466727.1; -;
 DR EMBL; X98100; CA466728.1; -;
 DR EMBL; AF124984; AAD18054.1; -;
 DR EMBL; AF148850; AAD37412.1; -;
 DR PIR; A44996; A44996.
 DR PDB; 1SHV; 05-MAY-99.
 DR PDB; 1G56; 14-FEB-01.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PRINTS; PR00118; BIACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolyase; Antibiotic resistance; Plasmid; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 286 BETA-LACTAMASE SHV-1.
 FT ACT_SITE 66 66
 FT BINDING 73 119
 FT BINDING 232 232
 FT CONFLICT 112 112 G -> A (IN REF. 1).
 FT CONFLICT 136 137 AT -> TA (IN REF. 5).
 FT CONFLICT 188 189 XL -> NVG (IN REF. 1).
 FT CONFLICT 278 278 A -> K (IN REF. 1).
 FT CONFLICT 281 281 I -> Y (IN REF. 1).
 FT HELIX 25 36
 FT HELIX 37 37
 FT STRAND 39 46
 FT STRAND 47 49
 FT STRAND 52 56
 FT STRAND 58 59
 FT STRAND 62 63
 FT STRAND 65 67
 FT HELIX 68 81
 FT HELIX 82 83
 FT TURN 87 88
 FT STRAND 90 91
 FT TURN 95 97
 FT HELIX 103 104
 FT TURN 105 108
 FT TURN 109 111

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RT STRAND 113 114
FT HELIX 115 124
FT HELIX 128 137
FT TURN 138 139
FT HELIX 140 150
FT TURN 151 152
FT STRAND 157 157
FT TURN 162 163
FT HELIX 164 166
FT TURN 170 171
FT TURN 174 175
FT STRAND 176 177
FT HELIX 179 191
FT TURN 193 194
FT HELIX 197 208
FT TURN 209 209
FT HELIX 214 220
FT TURN 223 224
FT STRAND 226 233
FT TURN 236 237
FT STRAND 239 246
FT TURN 248 249
FT STRAND 253 260
FT HELIX 266 282
FT TURN 283 283
SQ SEQUENCE 286 AA; 31224 MW; C78F42667E698B6C CRC64;
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Query Match 70.0%; Score 942; DB 1; Length 286;
Best Local Similarity 68.3%; Pred. No. 1.5e-67;
Matches 179; Conservative 38; Mismatches 45; Indels 0; Gaps 0;
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QY 2 PETLVKVDADQDQGVARYGTELDLNSGELLESPFSRSEFPFPMSTFKVLGCAVLSRIDA 61
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DB 23 PQLPRLQKLSQSSQSGRGVMEMLDASGRTLTAMRADRFPMSTFKVLGCAVLARDA 82
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 62 GQEQIGRIHYSDNLYVEVPYTEKRLTDGMTRELCASAITMSDNTANILLTTGGPK 121
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 83 GDEQLERKIHQQDLVYSPVSEKHLADGMTVVELCAAITMSDNSANILLATVGGPA 142
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 122 ELTAPLHNMGDHVTFLDWEPEPLNPAIPNDERDITTPVAMATTAKLTGELLTLASRQ 181
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 143 GLTAFRLQIGDNVTFLDWEPEPLNPAIPNDERDITTPVAMATTAKLTGELLTLASRQ 202
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 182 LIDWNEADKVAGELLRSALPAGFTADSGAGERSRGIIALGPGKPSRIVVITYTGS 241
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 203 LIDWNEADKVAGELLRSALPAGFTADSGAGERSRGIIALGPGKPSRIVVITYTGS 262
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 242 QATMDERNKQIAEIGASLIKHW 263
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 263 PASMAERNQIAGIGALIEHW 284
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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RESULT 3
BL13_KLEPN STANDARD; PRT; 286 AA.
AC Q9S424:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-lactamase SHV-13 precursor (EC 3.5.2.6).
GN BLA OR SHV13.
OS Klebsiella pneumoniae.
OC Plasmid.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=803;
RX MEDLINE=20187177; PubMed=10722518;
RA Yuan M., Hall J.M.C., Savellkoul P.H.M., Vandenbroucke-Grauls C.M.J.E.,
RA Livermore D.M.;
RT "SHV-13, a novel extended-spectrum beta-lactamase, in Klebsiella
```

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RT pneumoniae isolates from patients in an intensive care unit in
RT Amsterdam."
RL Antimicrob. Agents Chemother. 44:1081-1084(2000).
CC -1- FUNCTION: Broad spectrum beta-lactamase which hydrolyzes
CC penicillins, as well as cephalosporins except cephamycins. Also
CC hydrolyzes aztreonam, but not imipenem. Confers highly resistance
CC to ceftazidime, cefotaxime, aztreonam and piperacillin.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- ENZYME REGULATION: Inhibited 16-fold better by the beta-lactamase
CC inhibitor clavulanic acid than by tazobactam.
CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
```

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```

CC EMBL: AF164577; AAD43815.1; -.

DR HSSP; P14557; 1SHV

DR InterPro; IPR001466; Beta_lactamase.

DR InterPro; IPR000871; Beta_lactamase_A.

DR Pfam; PF00144; Beta_lactamase_1.

DR PRINTS; PRO0118; BLACTAMASEA.

DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.

KW Hydrolyase; Antibiotic resistance; Signal; Plasmid.

FT SIGNAL 1 21 POTENTIAL

FT CHAIN 22 286 BETA_LACTAMASE SHV-13.

FT ACT SITE 66 66 BY SIMILARITY.

FT DISULFID 73 119 BY SIMILARITY.

FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).

FT SEQUENCE 286 AA; 31253 MW; CBBF426D33FE502 CRC64;

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Query Match 69.9%; Score 940; DB 1; Length 286;
Best Local Similarity 67.9%; Pred. No. 2.1e-67;
Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;
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QY 2 PETLVKVDADQDQGVARYGTELDLNSGELLESPFSRSEFPFPMSTFKVLGCAVLSRIDA 61
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 23 PQLPRLQKLSQSSQSGRGVMEMLDASGRTLTAMRADRFPMSTFKVLGCAVLARDA 82
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 62 GQEQIGRIHYSDNLYVEVPYTEKRLTDGMTRELCASAITMSDNTANILLTTGGPK 121
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 83 GDEQLERKIHQQDLVYSPVSEKHLADGMTVVELCAAITMSDNSANILLATVGGPA 142
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 122 ELTAPLHNMGDHVTFLDWEPEPLNPAIPNDERDITTPVAMATTAKLTGELLTLASRQ 181
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 143 GLTAFRLQIGDNVTFLDWEPEPLNPAIPNDERDITTPVAMATTAKLTGELLTLASRQ 202
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 182 LIDWNEADKVAGELLRSALPAGFTADSGAGERSRGIIALGPGKPSRIVVITYTGS 241
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 203 LIDWNEADKVAGELLRSALPAGFTADSGAGERSRGIIALGPGKPSRIVVITYTGS 262
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 242 QATMDERNKQIAEIGASLIKHW 263
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 263 PASMAERNQIAGIGALIEHW 284
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

```
RESULT 4
BLA8_ECOLI STANDARD; PRT; 286 AA.
AC Q08337;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-lactamase SHV-8 precursor (EC 3.5.2.6).
GN BLA OR SHV8.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
```



```
RA Bradford P.A.;
RT "Automated thermal cycling is superior to traditional methods for
RT nucleotide sequencing of biased genes."
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: This enzyme hydrolyzes cefotaxime, ceftazidime and other
CC broad spectrum cephalosporins.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. DIFFERS
CC IN ONLY ONE POSITION FROM SHV-1.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62115; CAA44025.1; -
DR EMBL; X53433; CAA37524.1; -
DR EMBL; X53817; CAA37813.1; -
DR EMBL; X84314; CAA59058.1; -
DR EMBL; M95179; AAA25526.1; -
DR EMBL; L47119; AAA5015.1; -
DR EMBL; X98102; CAA6730.1; -
DR EMBL; AF148851; AAD37413.1; -
DR PIR; A44998; A44998.
DR HSSP; P14557; 1SHV.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Antibiotic resistance; Plasmid; Signal.
FT SIGNAL 1 21
FT CHAIN 22 286
FT ACT SITE 66 66 BY SIMILARITY.
FT DISULFID 73 119 BY SIMILARITY.
FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).
FT VARIANT 31 31 L->Q (IN SHV-24).
SQ SEQUENCE 286 AA; 31254 MW; 738F426651F551A CRC64;

Query Match 69.6%; Score 936; DB 1; Length 286;
Best Local Similarity 67.9%; Pred. No. 4.4e-67;
Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVKVDADQLGARVGYELDINSGLIESFSESEFPWMSFVKVLCGAVLSRIDA 61
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 23 PQLPQIKLSQSQLSGRVGMIEMLASGRTLTAMRADERFPWMSFVKVLCGAVLARVDA 82
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 GGEQIGRRIHYSQNDLVESPYTEKHLTDGMYRELCSAATMSDNTANLLTTIGGPK 121
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 83 GGEQIERKIHVQDQVLVSPVSEKHLADGMYVELCAAAITMSDNSANLLATVGGPA 142
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 EITAFILHMGDHYTLDRWEPELNEALPNDERDTTTPVAMATTKRLTGLLTLASRQ 181
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 143 GILTAFLRQIGDVTLDRETELNEALPDARDTTTPASMAATLRLTLTQSLSARSQ 202
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LIDWNEADKYAGPLRSALPAGMFTADKSGAGERSGRTIALGPKRSRIVVITYTSS 241
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 LIQMWVDDVAGPLRSVLPAGMFTADKTAGERGARGIIVALLGPNKAKERIVVIYLRDT 262
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 CATMDERNQIAEIGASLIKHW 263
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 PASMAERNQIAGIGALIEHW 284
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
BL24 ECOLI STANDARD; PRT; 286 AA.
ID BL24 ECOLI
AC Q9S169;
DT 16-OCT-2001 (Rel. 40, Created)
```

```
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DR Beta-lactamase SHV-24 precursor (EC 3.5.2.6).
GN BLA OR SHV24.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK741;
RA Kurokawa H., Yagi T., Shibata N., Arakawa Y.;
RT "New SHV-derived extended-spectrum beta-lactamase gene."
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS
CC NOTABLY CEFOTAXIME AND CEFOTAZIDIME.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB023477; BAA84973.1; -
DR HSSP; P14557; 1SHV.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Antibiotic resistance; Signal.
FT SIGNAL 1 21
FT CHAIN 22 286
FT ACT SITE 66 66 BY SIMILARITY.
FT DISULFID 73 119 BY SIMILARITY.
FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 286 AA; 31166 MW; 5EA9990BCB0A9AF CRC64;

Query Match 69.5%; Score 935; DB 1; Length 286;
Best Local Similarity 67.9%; Pred. No. 5.3e-67;
Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVKVDADQLGARVGYELDINSGLIESFSESEFPWMSFVKVLCGAVLSRIDA 61
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 23 PQLPQIKLSQSQLSGRVGMIEMLASGRTLTAMRADERFPWMSFVKVLCGAVLARVDA 82
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 GGEQIGRRIHYSQNDLVESPYTEKHLTDGMYRELCSAATMSDNTANLLTTIGGPK 121
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 83 GGEQIERKIHVQDQVLVSPVSEKHLADGMYVELCAAAITMSDNSANLLATVGGPA 142
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 EITAFILHMGDHYTLDRWEPELNEALPNDERDTTTPVAMATTKRLTGLLTLASRQ 181
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 143 GILTAFLRQIGDVTLDRETELNEALPDARDTTTPASMAATLRLTLTQSLSARSQ 202
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LIDWNEADKYAGPLRSALPAGMFTADKSGAGERSGRTIALGPKRSRIVVITYTSS 241
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 LIQMWVDDVAGPLRSVLPAGMFTADKTAGERGARGIIVALLGPNKAKERIVVIYLRDT 262
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 CATMDERNQIAEIGASLIKHW 263
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 PASMAERNQIAGIGALIEHW 284
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
BLA3 KLEPN STANDARD; PRT; 286 AA.
ID BLA3 KLEPN
AC P30856;
DT 01-UTL-1993 (Rel. 26, Created)
```

DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Beta-lactamase SHV-3 precursor (BC 3.5.2.6).
 GN BIA OR SHV3.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 ON NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9014623; PubMed=2694951.
 RA Nicolas M.H., Jarlier V., Honore N., Philippou A., Cole S.T.;
 RT "Molecular characterization of the gene encoding SHV-3 beta-lactamase
 responsible for transferable cefotaxime resistance in clinical
 isolates of Klebsiella pneumoniae." 1989.
 RT Antimicrob. Agents Chemother. 33:2096-2100(1989).
 CC -1- FUNCTION: This enzyme hydrolyzes cefotaxime, ceftazidime and other
 broad spectrum cephalosporins.
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 amino acid.
 CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
 DR PIR: A37200; A37200.
 DR HSSP: P14557; ISHV.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolyase; Antibiotic resistance; Plasmid; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 286 BETA-LACTAMASE SHV-3.
 FT ACT SITE 66 66 BY SIMILARITY.
 FT DISULFID 73 119 BY SIMILARITY.
 FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).
 FT SEQUENCE 286 AA; 31211 MW; 82715D986508F50D CRC64;
 SQ
 Query Match 69.4%; Score 933; DB 1; Length 286;
 Best Local Similarity 67.9%; Pred. No. 7,7e-67;
 Matches 178; Conservative 37; Mismatches 47; Indels 0; Gaps 0;
 QY 2 PETLVKVAEDQGLGARVGYELDLSNGELISFSEBEPFPMSTFKVLGCAVLSRIDA 61
 DB 23 PQLBQIKLSEQLSGRVGMIEMDLASGRTLTAMRADERPMMSTFKVLCGAVLARVDA 82
 QY 62 GGOQLGRRIHYSQNDIVESPYTEKRLTDGMTVRELSAATMSDVTANLITTTGGPK 121
 DB 83 GDEQLERKIHYSQNDIVESPYTEKRLTDGMTVRELSAATMSDVTANLITTTGGPK 142
 QY 122 ELTAFIHNAGDHYTRLDRWEPELEINAIPIVDERDTPVMAATLRLTLLGELLTLASRQ 181
 DB 143 GUTAFIHLQIGDVTYRLDRKMETELNEALPDARDTTPASMAATLRLTLLSQRLSARSQ 202
 QY 182 LIDWEADYVAGFLINSALPAGWFIADKSGAGRGSGIITAAIGPDGKPSRIVITTTGS 241
 DB 203 LIQWVDDVAGPLILRSVLPAGWFIADKSGAGRGSGIITAAIGPDGKPSRIVITTTGS 262
 QY 242 QATMDERNQIAETIGSLIKHW 263
 DB 263 PASMAERNQIAGIAGALIEHW 284
 RESULT 8
 BLAS KLEPN STANDARD; PRT; 286 AA.
 AC P37320;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-lactamase SHV-5 precursor (EC 3.5.2.6).
 GN BIA OR SHV5.
 OS Klebsiella pneumoniae, and
 OS Pseudomonas aeruginosa.
 OG Plasmid pPAG-KE.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 ON NCBI_TaxID=573, 287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91207045; PubMed=2086203;
 RA Billot-Klein D., Gutmann L., Collatz E.;
 RT "Nucleotide sequence of the SHV-5 beta-lactamase gene of a Klebsiella
 pneumoniae plasmid." 1990.
 RT Antimicrob. Agents Chemother. 34:2439-2441(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX SPECIES=K.pneumoniae; STRAIN=KPG-2, and KPLA-4;
 RX MEDLINE=97291235; PubMed=9145849;
 RA Niesch-Indenbien M., Kayser F.H., Hachler H.;
 RT "Survey and molecular genetics of SHV beta-lactamases in
 Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and
 SHV-12." 1997.
 RT Antimicrob. Agents Chemother. 41:943-949(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.aeruginosa;
 RA Sconlica E., Aransay A., Tselentis I.;
 RT "Extended spectrum beta-lactamase SHV-5 in Pseudomonas aeruginosa
 clinical strain." 1998.
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS
 NOTABLY CEFOTAXIME AND CEFOTAZIDIME. SHV-5 CAUSES PARTICULARLY HIGH
 LEVELS OF RESISTANCE TO AZTREONAM AND CERTAZIDIME.
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 amino acid.
 CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
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 or send an email to license@isb-sib.ch).
 CC EMBL: X56640; CAA39164.1; -
 CC EMBL: X98103; CAA66731.1; -
 CC EMBL: X98104; CAA66732.1; -
 CC EMBL: AF096930; AAC64608.1; -
 DR PIR: A60632; A60632.
 DR HSSP: P14557; ISHV.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta-lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolyase; Antibiotic resistance; Plasmid; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 286 BETA-LACTAMASE SHV-5.
 FT ACT SITE 66 66 BY SIMILARITY.
 FT DISULFID 73 119 BY SIMILARITY.
 FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).
 FT SEQUENCE 286 AA; 31253 MW; 738F426CC51F5FBA CRC64;
 SQ
 Query Match 69.3%; Score 932; DB 1; Length 286;
 Best Local Similarity 67.6%; Pred. No. 9,2e-67;
 Matches 177; Conservative 39; Mismatches 46; Indels 0; Gaps 0;
 QY 2 PETLVKVAEDQGLGARVGYELDLSNGELISFSEBEPFPMSTFKVLGCAVLSRIDA 61
 DB 23 PQLBQIKLSEQLSGRVGMIEMDLASGRTLTAMRADERPMMSTFKVLCGAVLARVDA 82
 QY 62 GGOQLGRRIHYSQNDIVESPYTEKRLTDGMTVRELSAATMSDVTANLITTTGGPK 121
 DB 83 GDEQLERKIHYSQNDIVESPYTEKRLTDGMTVRELSAATMSDVTANLITTTGGPK 142

Db 106 QSVASIKEMLVTSPTIKESLSPETVTEGKICQAASVSNDTANVVDALIGATGNAY 165
 QY 127 LHMNDGIVTRLDREPEPEINEAI PNDEPDTTPVMAATTLKLTGELLITLASRQOLIDWM 186
 Db 166 MRSIGDEETQIDREPEPEINEAI PNDEPDTTPVMAATTLKLTGELLITLASRQOLIDWM 225
 QY 187 EADVAGPELRSALPAGWFIADKSGAGERSGRIIALGPDGKRSRIYVITTSQATMD 246
 Db 226 LIDQVAGALLRASIPSWKILADKTGAGGYGSRSTIAVWPSPKQPLVVGITYITQTAKSMQ 285
 QY 247 ERNRQIAEIGASL 259
 Db 286 ASNOAIRIGVVL 298

RESULT 15
 BLG3_PSEAE
 ID BLG3_PSEAE STANDARD; PRT; 288 AA.
 AC P3732;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-lactamase CARB-3 precursor (EC 3.5.2.6) (Carbenicillinase 3).
 GN CARB3.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxId=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C106; TRANSPOSON=Tn1408;
 RX MEDLINE=91323732; PubMed=1650733;
 RA Lachapelle J., Dufrene J., Levesque R.C.;
 RT "Characterization of the blaCARB-3 gene encoding the
 RL carbenicillinase-3 beta-lactamase of Pseudomonas aeruginosa";
 RL Gene 102:7-12(1991).
 CC -1- FUNCTION: HYDROLYZES BOTH CARBENICILLIN AND OXACILLIN.
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S46063; AAB19430.2; ALT_INIT.
 CC PIR: J01136; J01136.
 CC DR HSP; P14557; ISHV.
 CC DR InterPro; IPR001466; Beta_lactamase.
 CC DR InterPro; IPR000871; Beta_lactamase_A.
 CC Pfam; PF00144; beta-lactamase; 1.
 CC DR PRINTS; PR00118; BLACTAMASEA.
 CC DR PROSITE; PS00146; BETA_LACTAMASE_A. 1.
 CC KW Hydrolyase; Antibiotic resistance; Signal; Transposable element.
 CC FT SIGNAL 1 17 POTENTIAL.
 CC FT CHAIN 1 288 BETA-LACTAMASE CARB-3.
 CC FT ACT SITE 65 65 BY SIMILARITY.
 CC FT DISULFID 72 118 BY SIMILARITY.
 CC FT BINDING 229 231 SUBSTRATE (BY SIMILARITY).
 CC SQ SEQUENCE 288 AA; 31313 MM; 38EAF8789201AC6 CRC64;

Query Match 40.1%; Score 539.5; DB 1; Length 288;
 Best Local Similarity 46.0%; Pred. No. 1.2e-35;
 Matches 116; Conservative 42; Mismatches 93; Indels 1; Gaps 1;

QY 8 VQDAEDQAGVGYEIDLSNGSILSFRSEFPFPMSTFYVLLCGAVLSRIDAGQEQDGL 67
 Db 29 VVAIEVSLARIGVSLDTQNGEYMD-YNGNQRFPLTSTFKTIACAKILYDAEGKVNN 87

QY 68 RRIHYSQNDLVEYSPTVEKHLTDGMVRELSAAITMSDNTANLITTTGGPEKELTAFL 127
 Db 88 STEVIEKADIVTSPTVEKQVQALITLDDACFAITMTSDNTANLITLAVGGEKGVDFL 147
 QY 128 HNMGDVTRLDREPEPEINEAI PNDEPDTTPVMAATTLKLTGELLITLASRQOLIDWM 187
 Db 148 RQIGDETRLDREPEPEINEAI PNDEPDTTPVMAATTLKLTGELLITLASRQOLIDWM 207
 QY 188 ADVAGPELRSALPAGWFIADKSGAGERSGRIIALGPDGKRSRIYVITTSQATMD 247
 Db 208 NNGVTGNLRSVLPAGWNIADRSAGAGFGARSITAVVMSHQAPIVSIYLAQTQASMAE 267
 QY 248 ERNRQIAEIGASL 259
 Db 268 RNDIVIKGHSI 279

Search completed: June 18, 2004, 19:08:28
 Job time : 18 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:59:13 ; Search time 21 Seconds

(without alignments)
1204.684 Million cell updates/sec

Title: EPPER526106.PEP

Sequence: 1 hpetlvkvkaedqlgary.....tmdermqtaeigaslkhk 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1330	98.9	286	S47061	beta-lactamase (EC
2	1330	98.9	286	T51301	beta-lactamase (EC
3	1330	98.9	286	S41975	beta-lactamase (EC
4	1325	98.5	286	PNECP	beta-lactamase (EC
5	1325	98.5	286	I40905	beta-lactamase (EC
6	1312	97.5	286	S60312	extended spectrum
7	1311	97.5	286	S30113	beta-lactamase (EC
8	1305	97.0	286	S60310	extended spectrum
9	1303	96.9	286	S60311	beta-lactamase (EC
10	1299	96.6	286	J01546	Bla protein - Salim
11	942	70.0	265	S00464	beta-lactamase (EC
12	940	69.9	286	S16146	beta-lactamase (EC
13	940	69.9	286	A66679	beta-lactamase (EC
14	936	69.6	265	S02434	beta-lactamase (EC
15	936	69.6	286	A44958	beta-lactamase (EC
16	933	69.4	286	A37200	beta-lactamase (EC
17	932	69.3	286	A60632	beta-lactamase (EC
18	929	69.1	265	A60448	beta-lactamase (EC
19	907.5	67.5	287	A44996	beta-lactamase (EC
20	897	66.7	279	A24469	beta-lactamase (EC
21	874	65.0	286	A44958	beta-lactamase (EC
22	672	50.0	298	A41381	beta-lactamase (EC
23	539.5	40.1	288	J01136	beta-lactamase (EC
24	539.5	40.1	304	A35001	beta-lactamase (EC
25	539.5	39.8	304	A49789	beta-lactamase (EC
26	529.5	39.4	288	U69755	beta-lactamase (EC
27	524.5	39.0	281	D93395	probable Beta lact
28	524	39.0	105	UC2566	bla protein - Pseu
29	521	38.7	276	JH0268	beta-lactamase (EC

30	513.5	38.2	291	2	S42075	beta-lactamase (EC
31	512.5	38.1	293	2	A54543	beta-lactamase (EC
32	512.5	38.1	293	2	S04649	beta-lactamase (EC
33	505.5	37.6	302	2	S36188	beta-lactamase (EC
34	496.5	36.9	294	2	S16553	beta-lactamase (EC
35	494.5	36.8	306	1	B45822	beta-lactamase (EC
36	489.5	36.5	291	2	JF0074	beta-lactamase (EC
37	489.5	36.4	305	2	A60680	beta-lactamase (EC
38	489.5	36.4	305	2	A57002	beta-lactamase (EC
39	489.5	36.4	305	2	A61156	beta-lactamase (EC
40	483.5	35.9	314	2	G69674	beta-lactamase (EC
41	483	35.9	306	2	S06967	beta-lactamase (EC
42	482.5	35.9	306	2	S47330	penicillinase - Ba
43	477	35.5	263	2	S23929	beta-lactamase (EC
44	471.5	35.1	294	2	S19006	beta-lactamase (EC
45	467.5	34.8	309	2	JC4117	beta-lactamase (EC

ALIGNMENTS

RESULT 1
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C/Spect: phage phi-X174
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C/Accession: S47061
R/Henrich, B.; Schmidberger, B.
Submitted to the EMBL Data Library, July 1994
A/Description: A variant of phix174 gene E-based positive selection vectors with enhance
A/Reference number: S47060
A/Accession: S47061
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <HEN>
A/Cross-references: EMBL:235638; NID:g520996; PIDN:CAA84692.1; PID:g520998
C/Superfamily: beta-lactamase I
C/Keywords: hydrolase

Query Match
Best Local Similarity 98.9%; Score 1330; DB 2; Length 286;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	HEETLVKVDADQDQARVGYIELDINSGEILSEFSERFPFMSFFKYLICGAVLSRID	60
DB	24	HEETLVKVDADQDQARVGYIELDINSGEILSEFSERFPFMSFFKYLICGAVLSRID	83
QY	61	AGQEQGRRIHYSQNDIVFYSVTEKHLTDGMTVARELCSAATMSDNTANLLITIGGP	120
DB	84	AGQEQGRRIHYSQNDIVFYSVTEKHLTDGMTVARELCSAATMSDNTANLLITIGGP	143
QY	121	KELTAFILHMGDVTPLDRWEPELNEAIPNDRDITTPVAMATTLRKLTGELLTLASRQ	180
DB	144	KELTAFILHMGDVTPLDRWEPELNEAIPNDRDITTPVAMATTLRKLTGELLTLASRQ	203
QY	181	QIDWMEADKVAGPLLRGALPAWFTADKSGAGRGSRGIIAALGPDGKPSRIWYITYG	240
DB	204	QIDWMEADKVAGPLLRGALPAWFTADKSGAGRGSRGIIAALGPDGKPSRIWYITYG	263
QY	241	SOATMDERNROIAETIGASLIKHW	263
DB	264	SOATMDERNROIAETIGASLIKHW	286

RESULT 2
T51301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C/Spect: Schizosaccharomyces pombe
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C/Accession: T51301
R/WACH, A.; BRACHAT, A.; ALBERTISEGUT, C.; REBISCHUNG, C.; PHILIPSEN, P.
Yeast 13, 1065-1075, 1997
A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharo

A:Reference number: Z09587
A:Accession: T51301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <MAC>
A:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C:Genetics:
A:Gene: bla
C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 98.9%; Score 1330; DB 2; Length 286;
Best Local Similarity 98.9%; Pred. No. 3.5e-103;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 60
DB HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 83
QY 61 AGOEOIGRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 120
DB AGOEOIGRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 180
DB KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203
QY 144 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLIRSAIPAGMTIADKSGAGERSGRTIATGPDGPKSRIVITTTG 240
DB QLIDWMEADKVAQPLIRSAIPAGMTIADKSGAGERSGRTIATGPDGPKSRIVITTTG 263
QY 241 SOATMDERNROIATIGASLIXHW 263
DB SOATMDERNROIATIGASLIXHW 286

RESULT 3
S41975
beta-lactamase (EC 3.5.2.6) precursor - synthetic
C:Species: synthetic
C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
C:Accession: S41975
R:Kaestner, K.H.; Montolju, L.; Kern, H.; Thulke, M.; Schutz, G.
Gene 148, 67-70, 1994
A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar
A:Reference number: A57991; MUID:95011660; PMID:7926839
A:Accession: S41975
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <KAS>
A:Cross-references: EMBL:X76682; NID:9453622; PIDN:CAA54104.1; PID:9453623
A>Note: submitted to the EMBL Data Library, December 1993
C:Keywords: hydrolase

Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 3.5e-103;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 60
DB HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 83
QY 24 HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 83
QY 61 AGOEOIGRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 120
DB AGOEOIGRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 143
QY 84 AGOEOIGRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 143
DB KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203
QY 121 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 180
DB KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203
QY 144 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203
DB QLIDWMEADKVAQPLIRSAIPAGMTIADKSGAGERSGRTIATGPDGPKSRIVITTTG 240
QY 181 QLIDWMEADKVAQPLIRSAIPAGMTIADKSGAGERSGRTIATGPDGPKSRIVITTTG 240
DB QLIDWMEADKVAQPLIRSAIPAGMTIADKSGAGERSGRTIATGPDGPKSRIVITTTG 263

QY 241 SOATMDERNROIATIGASLIXHW 263
DB SOATMDERNROIATIGASLIXHW 286

RESULT 4
PNECP
beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids
N:Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase
C:Species: Escherichia coli
C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 21-Jul-2000
C:Accession: A93821; A93820; A93817; S24415; A01005
R:Stutcliffe, U.G.
Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasm
A:Reference number: A93821; MUID:79012484; PMID:358200
A:Accession: A93821
A:Molecule type: DNA
A:Residues: 1-286 <SUT>
A:Cross-references: GB:V00613; GB:J01832; NID:943710; PIDN:CAA23886.1; PID:943713
A:Experimental source: plasmid pBR322
R:ambler, R.P.; Scott, G.K.
Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid
A:Reference number: A93820; MUID:79012483; PMID:358199
A:Accession: A93820
A:Molecule type: protein
A:Residues: 24-36, 'K', 38-286 <AMB>
A:Experimental source: plasmid R6K
R:Kornacki, J.A.; Buriage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990
A:Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence, poly
A:Reference number: A93817; MUID:90264294; PMID:2160936
A:Accession: A93817
A:Molecule type: DNA
A:Residues: 182-286 <KOR>
A:Cross-references: GB:M32794; NID:9152521; PIDN:AAA26408.1; PID:9152522
A:Experimental source: P82
R:Goussard, S.; Sougkoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
J. Gen. Microbiol. 137, 2681-2687, 1991
A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectru
A:Reference number: S24415; MUID:92166702; PMID:1665171
A:Accession: S24415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>
A:Cross-references: EMBL:X57972; NID:941816; PIDN:CAA41038.1; PID:941817
A:Experimental source: ISI-like blaT-6 DNA
R:Stutcliffe, U.G.
Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
A:Reference number: A90923; MUID:80002802; PMID:383387
A:Contents: annotation
C:Comment: like most penicillinases from gram-negative bacteria, this enzyme, coded by a
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase; membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:24-286/Product: beta-lactamase #status experimental <MAT>
F:68/Active site: Ser #status predicted
F:75-121/Dissulfide bonds: #status predicted

Query Match 98.5%; Score 1325; DB 1; Length 286;
Best Local Similarity 98.1%; Pred. No. 9.1e-103;
Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 60
DB HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 83
QY 24 HPEITLVKVDADQICARVGYIELDINSGETLIESPERSERFPMMSTFFKYLICGAVLSRD 83
DB AGOEOIGRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 120

Db 84 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
|||
Qy 121 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 180
|||
Db 144 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 203
|||
Qy 181 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 240
|||
Db 204 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 263
|||
Qy 241 SQATMDERNRQIAETIGASLIKHW 263
|||
Db 264 SQATMDERNRQIAETIGASLIKHW 286
|||

RESULT 5

I40905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A:Note: cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*
C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: I40905
R:Taylor, U.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 241-244, 1993
A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A:Reference number: I40904; MWID:93361581; PMID:769234
A:Accession: I40905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RES>
A:Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958
C:Keywords: hydrolase

Query Match 98.5%; Score 1325; DB 4; Length 286;
Best Local Similarity 98.1%; Pred. No. 9.1e-103;
Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQOLGARVGYIELDINSGEILSFSESEFPFPMSTFKVLLCGAVLSRID 60
|||
Db 24 HPEITLVKVDADQOLGARVGYIELDINSGEILSFSESEFPFPMSTFKVLLCGAVLSRID 83
|||
Qy 61 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
|||
Db 84 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
|||
Qy 121 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 180
|||
Db 144 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 203
|||
Qy 181 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 240
|||
Db 204 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 263
|||
Qy 241 SQATMDERNRQIAETIGASLIKHW 263
|||
Db 264 SQATMDERNRQIAETIGASLIKHW 286
|||

RESULT 6

S60312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, D.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MWID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:g296955; PIDN:CAA46346.1; PID:g296956
C:Superfamily: beta-lactamase I

Query Match 97.5%; Score 1312; DB 2; Length 286;
Best Local Similarity 97.0%; Pred. No. 1.1e-101;
Matches 255; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQOLGARVGYIELDINSGEILSFSESEFPFPMSTFKVLLCGAVLSRID 60
|||
Db 24 HPEITLVKVDADQOLGARVGYIELDINSGEILSFSESEFPFPMSTFKVLLCGAVLSRID 83
|||
Qy 61 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
|||
Db 84 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
|||
Qy 121 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 180
|||
Db 144 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 203
|||
Qy 181 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 240
|||
Db 204 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 263
|||
Qy 241 SQATMDERNRQIAETIGASLIKHW 263
|||
Db 264 SQATMDERNRQIAETIGASLIKHW 286
|||

RESULT 7

S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFE04
C:Species: *Klebsiella pneumoniae*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: S30113
R:Mabiat, C.; Lourenco-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between *Tn1* and *Tn21*: the antibiotic multiple
A:Reference number: S30112; MWID:93062798; PMID:1331747
A:Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>

A:Cross-references: EMBL:X64523; NID:g43797; PIDN:CAA45628.1; PID:g43798
C:Keywords: antibiotic resistance; hydrolase
C:Superfamily: beta-lactamase I

Query Match 97.5%; Score 1311; DB 2; Length 286;
Best Local Similarity 97.0%; Pred. No. 1.3e-101;
Matches 255; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQOLGARVGYIELDINSGEILSFSESEFPFPMSTFKVLLCGAVLSRID 60
|||
Db 24 HPEITLVKVDADQOLGARVGYIELDINSGEILSFSESEFPFPMSTFKVLLCGAVLSRID 83
|||
Qy 61 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
|||
Db 84 AGGEOGRRRIHYSQNDLVKVSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
|||
Qy 121 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 180
|||
Db 144 KELTAFILHNMGDHVTRLDRWPEPELNBAIPNDRDITTPVAMATTIRKLLTGEILLTLASRQ 203
|||
Qy 181 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 240
|||
Db 204 QLIDMWEADKVAAGPLLRSAIPAGWFIADKSGAGERSGRTIAALGPDGKPSRIIVYITTG 263
|||
Qy 241 SQATMDERNRQIAETIGASLIKHW 263
|||
Db 264 SQATMDERNRQIAETIGASLIKHW 286
|||

```
RESULT 8
S60310
Extended spectrum beta-lactamase CAZ-2 - Klebsiella pneumoniae
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C/Accession: S60310
R/Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60310
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CHA>
A/Cross-references: EMBL:X65252; NID:g296951; PIDD:CAA6344.1; PID:g296952
C/Superfamily: beta-lactamase I

Query Match          97.0%; Score 1305; DB 2; Length 286;
Best Local Similarity 96.6%; Pred. No. 4.2e-101;
Matches 254; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 HPEITVVKYKADBDQAGRVGYIELDINSGEILIESFRSEERPPMSTFKVLLCGAVLSRID 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 24 HPEITVVKYKADBDQAGRVGYIELDINSGEILIESFRSEERPPMSTFKVLLCGAVLSRD 83
QY 61 AGOEQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 84 AGOEQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVANAATLTKLLTGELLTLASRQ 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 144 KELTAFILNMGDHVTRLDRWSPELNEAIPNDRDITTPVANAATLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 204 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNRQIAETIGASLTKHW 263
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 264 SOATMDERNRQIAETIGASLTKHW 286
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C/Accession: S60311; F37392; F00498
R/Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60311
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CHA>
A/Cross-references: EMBL:X65253; NID:g296953; PIDD:CAA6345.1; PID:g296954
R/Folmasy, M.E.
Plasmid 24, 218-226, 1990
A/Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans
A/Reference number: A37392; MUID:91172904; PMID:1963948
A/Accession: F37392
A/Molecule type: DNA
A/Residues: 1-32 <TOL>
A/Cross-references: GB:M55547; NID:g155010; PIDD:AAA98408.1; PID:g155016
C/Genetics:
A/Gene: TEM-bla
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match          96.9%; Score 1303; DB 2; Length 286;
Best Local Similarity 96.2%; Pred. No. 6.1e-101;
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Matches 253; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 HPEITVVKYKADBDQAGRVGYIELDINSGEILIESFRSEERPPMSTFKVLLCGAVLSRID 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 24 HPEITVVKYKADBDQAGRVGYIELDINSGEILIESFRSEERPPMSTFKVLLCGAVLSRD 83
QY 61 AGOEQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 84 AGOEQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVANAATLTKLLTGELLTLASRQ 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 144 KELTAFILNMGDHVTRLDRWSPELNEAIPNDRDITTPVANAATLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
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DB 204 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNRQIAETIGASLTKHW 263
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DB 264 SOATMDERNRQIAETIGASLTKHW 286
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RESULT 10
J01546
Bla protein - Salmonella typhimurium plasmid NTP16
N/Alternate names: beta lactamase homolog
C/Species: Salmonella typhimurium
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: J01546
R/Cannon, P.W.; Strike, P.
Plasmid 27, 220-230, 1992
A/Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A/Reference number: J01538; MUID:92383313; PMID:1325061
A/Accession: J01546
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CAN>
C/Genetics:
A/Genome: plasmid
C/Superfamily: beta-lactamase I

Query Match          96.6%; Score 1299; DB 2; Length 286;
Best Local Similarity 96.6%; Pred. No. 1.3e-100;
Matches 254; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 HPEITVVKYKADBDQAGRVGYIELDINSGEILIESFRSEERPPMSTFKVLLCGAVLSRID 60
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DB 24 HPEITVVKYKADBDQAGRVGYIELDINSGEILIESFRSEERPPMSTFKVLLCGAVLSRD 83
QY 61 AGOEQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
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DB 84 AGOEQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVANAATLTKLLTGELLTLASRQ 180
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DB 144 KELTAFILNMGDHVTRLDRWSPELNEAIPNDRDITTPVANAATLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
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DB 204 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNRQIAETIGASLTKHW 263
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 264 SOATMDERNRQIAETIGASLTKHW 286
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RESULT 11
S00464
beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453
N/Alternate names: beta-lactamase p453; beta-lactamase SHV-1
C/Species: Escherichia coli
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
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Query Match	69.9%	Score 940;	DB 2;	Length 286;
Best Local Similarity	67.9%	Pred. No. 1e-70;		
Matches 178;	Conservative 38;	Mismatches 46;	Indels 0;	Gaps 0

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Db      263 PASMARNQQTIGIGALIEHW 284
RESIDT 14

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S02434
beta-lactamase (EC 3.5.2.6) SHV-2 - Escherichia coli
C;Species: Escherichia coli
#Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text change 18-Jun-1993

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:09:08 ; Search time 49 Seconds

(without alignments)
1515.275 Million cell updates/sec

Title: EPPER526106.PEP
Perfect score: 1345
Sequence: 1 hpetlwkvdadqlgarvgy.....tmdermqiaiegaslikhw 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA:*
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11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330	98.9	263	12	US-10-668-778-2
2	1330	98.9	286	10	US-09-919-901-7
3	1330	98.9	286	10	US-09-919-901-14
4	1330	98.9	286	10	US-09-919-901-21
5	1330	98.9	286	12	US-09-837-306-354
6	1330	98.9	286	14	US-10-191-966-7
7	1330	98.9	286	14	US-10-191-966-14
8	1330	98.9	286	15	US-10-191-966-21
9	1330	98.9	286	15	US-10-045-674-523
10	1330	98.9	2307	10	US-09-919-901-2
11	1330	98.9	2307	10	US-09-919-901-9
12	1330	98.9	2307	10	US-09-919-901-16
13	1330	98.9	2307	14	US-10-191-966-2
14	1330	98.9	2307	14	US-10-191-966-9
15	1330	98.9	2307	14	US-10-191-966-16

16	1329	98.8	286	14	US-10-231-013-9	Sequence 9, Appl1
17	1329	98.8	1233	14	US-10-251-385-292	Sequence 292, App
18	1325	98.5	265	9	US-09-772-114-6	Sequence 6, Appl1
19	1325	98.5	265	14	US-10-280-482-2	Sequence 2, Appl1
20	1325	98.5	285	9	US-09-772-114-7	Sequence 7, Appl1
21	1325	98.5	286	14	US-10-016-668-5	Sequence 5, Appl1
22	1325	98.5	286	14	US-10-280-482-4	Sequence 4, Appl1
23	1322	98.3	352	16	US-10-469-199-2	Sequence 2, Appl1
24	1318	98.0	265	9	US-09-772-114-8	Sequence 8, Appl1
25	1318	98.0	265	14	US-10-280-482-6	Sequence 6, Appl1
26	1317	97.9	264	9	US-09-772-114-9	Sequence 9, Appl1
27	1317	97.9	264	14	US-10-280-482-8	Sequence 8, Appl1
28	1310.5	97.4	262	12	US-10-393-449-3	Sequence 3, Appl1
29	1310.5	97.4	262	14	US-10-177-725-3	Sequence 3, Appl1
30	1281	95.2	284	16	US-10-062-188-2	Sequence 2, Appl1
31	578	43.0	118	16	US-10-062-188-3	Sequence 3, Appl1
32	539.5	40.1	288	14	US-10-016-668-6	Sequence 6, Appl1
33	457	34.0	94	12	US-09-925-298-760	Sequence 760, App
34	457	34.0	94	14	US-10-102-806-760	Sequence 760, App
35	438.5	32.6	321	14	US-10-156-761-11986	Sequence 11986, A
36	433.5	32.2	251	16	US-10-062-188-1	Sequence 1, Appl1
37	392	29.1	262	9	US-09-772-114-10	Sequence 10, Appl1
38	392	29.1	262	14	US-10-280-482-10	Sequence 10, Appl1
39	175	13.0	290	16	US-10-414-532-65	Sequence 65, Appl1
40	137	10.2	334	10	US-09-894-159-4	Sequence 4, Appl1
41	137	10.2	841	10	US-09-894-159-2	Sequence 2, Appl1
42	109	8.1	21	16	US-10-414-532-3	Sequence 3, Appl1
43	107.5	8.0	524	16	US-10-414-532-28	Sequence 28, Appl1
44	106	7.9	68	12	US-10-424-599-175764	Sequence 175764,
45	97	7.2	561	12	US-10-425-114-73015	Sequence 73015, A

ALIGNMENTS

RESULT 1
US-10-668-778-2
; Sequence 2, Application US/10668778
; Publication No. US20040038317A1
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Kalobios, Inc.
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-000700US
; CURRENT APPLICATION NUMBER: US/10/668,778
; PRIOR APPLICATION NUMBER: US/09/526,106
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124,339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135,926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 98.9%; Score 1330; DB 12; Length 263;
Best Local Similarity 98.9%; Pred No. 6.5e-129;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITWKVDADQIGARVGYIELDINSGEILSFRSEERFPWMSIFKVLICGAVLSRID 60
DB 1 HPEITWKVDADQIGARVGYIELDINSGEILSFRSEERFPWMSIFKVLICGAVLSRID 60

Qy	61	AGGEOIGRRIRIHYSQNDIVAVSPVTEKHLTDGWTAVREICSAITMSDNTAANLLITTTGGP	120
Db	61	AGGEOIGRRIRIHYSQNDIVAVSPVTEKHLTDGWTAVREICSAITMSDNTAANLLITTTGGP	120
Qy	121	KELTALFELHNMGGHVTELRDWEPELNEALPNDERDITTTVPVAATTLTKLLTGELLTLASRQ	180
Db	121	KELTALFELHNMGGHVTELRDWEPELNEALPNDERDITTTVPVAATTLTKLLTGELLTLASRQ	180
Qy	181	QILDWMEADKVAAGPILRSALPGAWPLADKSGAGERSGIIITAAIGPDGKRSRIVVIYTTG	240
Db	181	QILDWMEADKVAAGPILRSALPGAWPLADKSGAGERSGIIITAAIGPDGKRSRIVVIYTTG	240
Qy	241	SOATMDERNRQIAETGASLITKH	263
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RESULT 2
US-09-919-901-7
Sequence 7, Application US/099199801
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OR INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OR INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-7

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Query Match	98.9%;	Score 1330;	DB 10;	Length 286;
Best Local Similarity	98.9%;	Pred. No. 7,36-129;		
Matches 260;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	HPETLVKVKDADDDQVGARVGYIELDLSNGETLESFRRSEERPEPMSTFKYLICGAVLSRID	60	
Db	24	HPETLVKVKDADDDQVGARVGYIELDLSNGKLTIESRPEERPEPMSTFKYLICGAVLSRID	83	
QY	61	AGQELGRRIHYSQNDLIVEYSPVTEKHLITDGMTVELCSAATIMSDNTAANLLTTIGGP	120	
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QY	121	KELTAFILNMGGDVTFLDRMEPELNEAIPNDRDITTPVAMATTLRKILITGELLTLASRQ	180	
Db	144	KELTAFILNMGGDVTFLDRMEPELNEAIPNDRDITTPVAMATTLRKILITGELLTLASRQ	203	
QY	181	QLIDMMEADKVAGPLIRSLPAGWTIADKSGGEGSGRGIITALGPDGKPSIVIVITTTG	240	
Db	204	QLIDMMEADKVAGPLIRSLPAGWFIADKSGGEGSGRGIITALGPDGKPSIIVIVITTTG	263	
QY	241	SOATMDERNRQIAELIGASLTIKHM	263	
Db	264	SOATMDERNRQIAELIGASLTIKHM	286	

RESULT 3
US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1

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GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-14

Query Match          98.9%      Score 1330; DB 10; Length 286;
Best Local Similarity 98.9%      Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

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Db	24	HPETLVKDKAMBDQIGARVGIETLIDNLSGKLLIESFRPEERFPMSSTFKYLLCGAVLSRID	83
QY	61	AGEQLGRRIHYSDNDLVEYSPVTEKHLLTDCMTVELCSAALTMSDNTANILLTTIGSP	120
Db	84	AGEQLGRRIHYSDNDLVEYSPVTEKHLLTDCMTVELCSAALTMSDNTANILLTTIGSP	143
QY	121	KEITLPEFLNMGDHYRLDRWPELNELAPNDRDPTTPPAMATTLTKLITGELLTLASRQ	180
Db	144	KEITLPEFLNMGDHYRLDRWPELNELAPNDRDPTTPPAMATTLTKLITGELLTLASRQ	203
QY	181	QLIDWMEADKVAGPLLRSLAPAGWETADKSGAGERSGIIAALGPDGKPSRIIVTYTTG	240
Db	204	QLIDWMEADKVAGPLLRSLAPAGWETADKSGAGERSGIIAALGPDGKPSRIIVTYTTG	263
QY	241	SOATMDERNRQIAETGASLIIKHW	263
Db	264	SOATMDERNRQIAETGASLIIKHW	286

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/ RESULT 4
/ US-09-919-901-21
/ Sequence 21, Application US/09913901
/ Publication No. US20030082518A1
/ GENERAL INFORMATION:
/ APPLICANT: Potts, Karen E.
/ APPLICANT: Jackson, Roberta L.
/ APPLICANT: Patrick, Amy K.
/ TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
/ TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
/ FILE REFERENCE: 0125-0005A
/ CURRENT APPLICATION NUMBER: US/09/919,901
/ CURRENT FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 09/263,933
/ PRIOR FILING DATE: 1999-02-08
/ PRIOR APPLICATION NUMBER: 09/129,611
/ PRIOR FILING DATE: 1998-08-05
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/
/ LENGTH: 286
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION:
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US-09-919-901-21

Query Match 98.9%; Score 1330; DB 10; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 24 HPELVKVAEDQAGRVYIELDLSNGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
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QY 61 AGGEOLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
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DB 84 AGGEOLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
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QY 121 KELLTAFLHNMGDVTRLDWEPELNEAIPNDERDITTPVAMATTLKLTGELLTASRQ 180
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QY 181 QLIDWMEADKVAAPLLRSALPAGMFIADKSGAGERSGRIIAGDPGKPSRIVITYTG 240
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DB 204 QLIDWMEADKVAAPLLRSALPAGMFIADKSGAGERSGRIIAGDPGKPSRIVITYTG 263
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QY 241 SQATMDERNQIAEIGASLIKHW 263
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DB 264 SQATMDERNQIAEIGASLIKHW 286
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RESULT 5

US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1

GENERAL INFORMATION:

; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROONEY, KRISTIN L.
; APPLICANT: HOBT, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRF
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCESS
US-09-837-306-354

Query Match 98.9%; Score 1330; DB 12; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 24 HPELVKVAEDQAGRVYIELDLSNGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
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QY 61 AGGEOLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
|||
DB 84 AGGEOLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
|||
QY 121 KELLTAFLHNMGDVTRLDWEPELNEAIPNDERDITTPVAMATTLKLTGELLTASRQ 180
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DB 144 KELLTAFLHNMGDVTRLDWEPELNEAIPNDERDITTPVAMATTLKLTGELLTASRQ 203
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QY 181 QLIDWMEADKVAAPLLRSALPAGMFIADKSGAGERSGRIIAGDPGKPSRIVITYTG 240
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DB 204 QLIDWMEADKVAAPLLRSALPAGMFIADKSGAGERSGRIIAGDPGKPSRIVITYTG 263
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QY 241 SQATMDERNQIAEIGASLIKHW 263
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DB 264 SQATMDERNQIAEIGASLIKHW 286
|||

RESULT 6

US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1

GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 98.9%; Score 1330; DB 14; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVAEDQAGRVYIELDLSNGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
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DB 24 HPELVKVAEDQAGRVYIELDLSNGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
|||
QY 61 AGGEOLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
|||
DB 84 AGGEOLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
|||
QY 121 KELLTAFLHNMGDVTRLDWEPELNEAIPNDERDITTPVAMATTLKLTGELLTASRQ 180
|||
DB 144 KELLTAFLHNMGDVTRLDWEPELNEAIPNDERDITTPVAMATTLKLTGELLTASRQ 203
|||
QY 181 QLIDWMEADKVAAPLLRSALPAGMFIADKSGAGERSGRIIAGDPGKPSRIVITYTG 240
|||
DB 204 QLIDWMEADKVAAPLLRSALPAGMFIADKSGAGERSGRIIAGDPGKPSRIVITYTG 263
|||
QY 241 SQATMDERNQIAEIGASLIKHW 263
|||
DB 264 SQATMDERNQIAEIGASLIKHW 286
|||

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: :
OTHER INFORMATION: :
US-10-191-966-14

Query Match 98.9%; Score 1330; DB 14; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVKVDAEDQIGARVGYIELDINSGEILIESFRSEPERPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKVDAEDQIGARVGYIELDINSGEILIESFRSEPERPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFINMGDHYRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGELTLASRQ 180
DB 144 KELTAFINMGDHYRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGELTLASRQ 203
QY 161 QIIMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QIIMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAETIGASLIKHW 263
DB 264 SOATMDERNROIAETIGASLIKHW 266

RESULT 8

US-10-191-966-21
Sequence 21, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 98.9%; Score 1330; DB 14; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVKVDAEDQIGARVGYIELDINSGEILIESFRSEPERPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKVDAEDQIGARVGYIELDINSGEILIESFRSEPERPMSTFKVLLCGAVLSRID 83

QY 61 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFINMGDHYRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGELTLASRQ 180
DB 144 KELTAFINMGDHYRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGELTLASRQ 203
QY 161 QIIMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QIIMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAETIGASLIKHW 263
DB 264 SOATMDERNROIAETIGASLIKHW 286

RESULT 9

US-10-045-674-523
Sequence 523, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOEFT, RENE
APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DVAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCRSS
US-10-045-674-523

Query Match 98.9%; Score 1330; DB 15; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.3e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVKVDAEDQIGARVGYIELDINSGEILIESFRSEPERPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKVDAEDQIGARVGYIELDINSGEILIESFRSEPERPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFINMGDHYRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGELTLASRQ 180
DB 144 KELTAFINMGDHYRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGELTLASRQ 203
QY 161 QIIMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QIIMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAETIGASLIKHW 263
DB 264 SOATMDERNROIAETIGASLIKHW 286

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RESULT 10
US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Karen E.
; APPLICANT: Potts, Karen B.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-2

Query Match          98.9%; Score 1330; DB 10; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDQAGRVGYIELDINSGEILSFSPSEERPFPMSTFKVLLCGAVLSRID 60
DB 2045 HPEITLVKVDADQDQAGRVGYIELDINSGEILSFSPSEERPFPMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTTGGP 120
DB 2105 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTTGGP 2164
QY 121 KETIAFLHNMGDHVTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGLLTLASRQ 180
DB 2165 KETIAFLHNMGDHVTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGLLTLASRQ 2224
QY 181 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGRGIALLGPDGKPSRIIVYTTG 240
DB 2225 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGRGIALLGPDGKPSRIIVYTTG 2284
QY 241 SOATMDERNRQIAEIGASLIKHM 263
DB 2285 SOATMDERNRQIAEIGASLIKHM 2307

RESULT 11
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
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; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9

Query Match          98.9%; Score 1330; DB 10; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDQAGRVGYIELDINSGEILSFSPSEERPFPMSTFKVLLCGAVLSRID 60
DB 2045 HPEITLVKVDADQDQAGRVGYIELDINSGEILSFSPSEERPFPMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTTGGP 120
DB 2105 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTTGGP 2164
QY 121 KETIAFLHNMGDHVTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGLLTLASRQ 180
DB 2165 KETIAFLHNMGDHVTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGLLTLASRQ 2224
QY 181 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGRGIALLGPDGKPSRIIVYTTG 240
DB 2225 QLIDWMEADKVAQPLIRSLPAGWFIADKSGAGERSGRGIALLGPDGKPSRIIVYTTG 2284
QY 241 SOATMDERNRQIAEIGASLIKHM 263
DB 2285 SOATMDERNRQIAEIGASLIKHM 2307

RESULT 12
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16

Query Match          98.9%; Score 1330; DB 10; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDQAGRVGYIELDINSGEILSFSPSEERPFPMSTFKVLLCGAVLSRID 60
DB 2045 HPEITLVKVDADQDQAGRVGYIELDINSGEILSFSPSEERPFPMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTTGGP 120
DB 2105 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTTGGP 2164
QY 121 KETIAFLHNMGDHVTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGLLTLASRQ 180
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Db 2165 KETLAFIHNMGDHYTRLDRMEPELNEAI PNDERDTTVMANATTKRLITGELTLASRQ 2224
Qy 181 QLIMMEADKVAGPLLSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIYTTG 240
Db 2225 QLIMMEADKVAGPLLSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIYTTG 2284
Qy 241 SQATMDERNROIAETGASLTKHW 263
Db 2285 SQATMDERNROIAETGASLTKHW 2307

RESULT 13
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-2

Query Match 98.9%; Score 1330; DB 14; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKKAEDQLGARVGYIELDINSGETLSEFRSEFRPMMSTFKVLICGAVLSRID 60
Db 2045 HPEITLVKKAEDQLGARVGYIELDINSGETLSEFRSEFRPMMSTFKVLICGAVLSRID 2104
Qy 61 AGOEOLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
Db 2105 AGOEOLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 2164
Qy 121 KETLAFIHNMGDHYTRLDRMEPELNEAI PNDERDTTVPAMATTKRLITGELTLASRQ 180
Db 2165 KETLAFIHNMGDHYTRLDRMEPELNEAI PNDERDTTVPAMATTKRLITGELTLASRQ 2224
Qy 181 QLIMMEADKVAGPLLSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIYTTG 240
Db 2225 QLIMMEADKVAGPLLSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIYTTG 2284
Qy 241 SQATMDERNROIAETGASLTKHW 263
Db 2285 SQATMDERNROIAETGASLTKHW 2307

RESULT 14
US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
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; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-9

Query Match 98.9%; Score 1330; DB 14; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKKAEDQLGARVGYIELDINSGETLSEFRSEFRPMMSTFKVLICGAVLSRID 60
Db 2045 HPEITLVKKAEDQLGARVGYIELDINSGETLSEFRSEFRPMMSTFKVLICGAVLSRID 2104
Qy 61 AGOEOLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
Db 2105 AGOEOLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 2164
Qy 121 KETLAFIHNMGDHYTRLDRMEPELNEAI PNDERDTTVPAMATTKRLITGELTLASRQ 180
Db 2165 KETLAFIHNMGDHYTRLDRMEPELNEAI PNDERDTTVPAMATTKRLITGELTLASRQ 2224
Qy 181 QLIMMEADKVAGPLLSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIYTTG 240
Db 2225 QLIMMEADKVAGPLLSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIYTTG 2284
Qy 241 SQATMDERNROIAETGASLTKHW 263
Db 2285 SQATMDERNROIAETGASLTKHW 2307

RESULT 15
US-10-191-966-16
; Sequence 16, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-16

Query Match 98.9%; Score 1330; DB 14; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      1 HPETIVKVDADQDQGVGYIELDINSGEILSPFRSEERFPMMSTFKVLLCGAVLSRID 60
Db      2045 HPETIVKVDADQDQGVGYIELDINSGEILSPFRSEERFPMMSTFKVLLCGAVLSRID 2104
QY      61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANLITTTIGP 120
Db      2105 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANLITTTIGP 2164
QY      121 KETLAFIHNMGDVTRLDRWEPELNEAI PNDERDITTPVAMATTIRKLTGELLITLASRQ 180
Db      2165 KETLAFIHNMGDVTRLDRWEPELNEAI PNDERDITTPVAMATTIRKLTGELLITLASRQ 2224
QY      181 QLDWMEADKVAGPILRSALPAGMTADKSGAGRGSGIILAIGPDGKPSRIWVYTTG 240
Db      2225 QLDWMEADKVAGPILRSALPAGMTADKSGAGRGSGIILAIGPDGKPSRIWVYTTG 2284
QY      241 SQATMDERNRQIAEIGASLIKHW 263
Db      2285 SQATMDERNRQIAEIGASLIKHW 2307

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Search completed: June 18, 2004, 19:15:27
 Job time : 51 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:06:58 ; Search time 22 Seconds

(Without alignments)
617.165 Million cell updates/sec

Title: EPPER526106.PEP

Perfect score: 1345

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
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4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1330	98.9	286	1	US-08-339-658-2
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4	1330	98.9	286	3	US-09-263-933-14
5	1330	98.9	286	3	US-09-263-933-21
6	1330	98.9	286	4	US-09-025-769B-265
7	1330	98.9	286	4	US-09-025-769B-362
8	1330	98.9	286	4	US-09-919-901-7
9	1330	98.9	286	4	US-09-919-901-14
10	1330	98.9	286	4	US-09-919-901-21
11	1330	98.9	286	4	US-09-025-769B-285
12	1330	98.9	286	4	US-09-025-769B-298
13	1330	98.9	286	4	US-09-025-769B-300
14	1330	98.9	286	3	US-09-263-933-2
15	1330	98.9	286	3	US-09-263-933-9
16	1330	98.9	286	3	US-09-263-933-16
17	1330	98.9	286	4	US-09-919-901-2
18	1330	98.9	286	4	US-09-919-901-9
19	1330	98.9	286	4	US-09-919-901-16
20	1330	98.9	286	4	US-09-555-510B-9
21	1330	98.9	286	4	US-09-170-496D-292
22	1330	98.9	286	4	US-09-364-425B-57
23	1330	98.9	286	4	US-08-407-544-2
24	1330	98.9	286	2	US-08-719-697-2
25	1330	98.9	286	2	US-08-727-616A-2
26	1330	98.9	286	4	US-09-481-756-2
27	1330	98.9	286	2	US-08-719-697-4

28	1325	98.5	286	3	US-08-727-616A-4	Sequence 4, Appli
29	1325	98.5	286	4	US-09-481-756-4	Sequence 4, Appli
30	1320	98.1	290	4	US-09-489-039A-11407	Sequence 11407, A
31	1318	98.0	265	2	US-08-719-697-6	Sequence 6, Appli
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34	1317	97.9	264	2	US-08-719-697-8	Sequence 8, Appli
35	1317	97.9	264	3	US-08-727-616A-8	Sequence 8, Appli
36	1317	97.9	264	4	US-09-481-756-8	Sequence 8, Appli
37	1310.5	97.4	262	4	US-09-626-581D-3	Sequence 3, Appli
38	1310.5	97.4	262	4	US-09-415-765B-3	Sequence 3, Appli
39	1310.5	97.4	262	4	US-09-626-580C-3	Sequence 3, Appli
40	1308	97.2	286	1	US-08-346-333-16	Sequence 16, Appli
41	1308	97.2	286	5	PCT-US91-07506-16	Sequence 16, Appli
42	942	70.0	313	4	US-09-489-039A-11425	Sequence 11425, A
43	499	37.1	142	4	US-09-489-039A-9803	Sequence 9803, Ap
44	446	33.2	247	4	US-09-489-039A-11509	Sequence 11509, A
45	441	32.8	192	4	US-09-489-039A-9460	Sequence 9460, Ap

ALIGNMENTS

RESULT 1
US-07-721-775A-2
Sequence 2, Application US/07721775A
Patent No. 5180666
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: Reising, Echington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48069
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07721,775A
FILING DATE: 19910627
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321MSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-07-721-775A-2

Query Match
Best Local Similarity 98.9%; Score 1330; DB 1; Length 286;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPECLTKVKAADQAGRVGYTELDINSGEILSEFRSEFRPFMSTFKYLGGAVLSRID 60
DB 24 HPECLTKVKAADQAGRVGYTELDINSGEILSEFRSEFRPFMSTFKYLGGAVLSRID 83

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QY 61 AGGOLGRRIHYSQNDLVEYSPYTERKHLTDGMYRELCSAATMSDNTANLLTTIGP 120
DB 84 AGGOLGRRIHYSQNDLVEYSPYTERKHLTDGMYRELCSAATMSDNTANLLTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMWEADKXAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 240
DB 204 QLIDMWEADKXAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 263
QY 241 SOATMDERNROIAEIGASLIIKH 263
DB 264 SOATMDERNROIAEIGASLIIKH 286

RESULT 2
US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5523482
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5525482ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Echington, Barnard, Perry & Milton
; STREET: P. O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321MSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQIGARVGYIELDNLNGSELLESFRSEERFPWMTFXYLGCAYLSRID 60
DB 24 HPEITLVKXDAEDQIGARVGYIELDNLNGSELLESFRSEERFPWMTFXYLGCAYLSRID 83
QY 61 AGGOLGRRIHYSQNDLVEYSPYTERKHLTDGMYRELCSAATMSDNTANLLTTIGP 120
DB 84 AGGOLGRRIHYSQNDLVEYSPYTERKHLTDGMYRELCSAATMSDNTANLLTTIGP 143
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QY 121 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMWEADKXAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 240
DB 204 QLIDMWEADKXAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 263
QY 241 SOATMDERNROIAEIGASLIIKH 263
DB 264 SOATMDERNROIAEIGASLIIKH 286

RESULT 3
US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-7

Query Match 98.9%; Score 1330; DB 3; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQIGARVGYIELDNLNGSELLESFRSEERFPWMTFXYLGCAYLSRID 60
DB 24 HPEITLVKXDAEDQIGARVGYIELDNLNGSELLESFRSEERFPWMTFXYLGCAYLSRID 83
QY 61 AGGOLGRRIHYSQNDLVEYSPYTERKHLTDGMYRELCSAATMSDNTANLLTTIGP 120
DB 84 AGGOLGRRIHYSQNDLVEYSPYTERKHLTDGMYRELCSAATMSDNTANLLTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMWEADKXAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 240
DB 204 QLIDMWEADKXAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 263
QY 241 SOATMDERNROIAEIGASLIIKH 263
DB 264 SOATMDERNROIAEIGASLIIKH 286

RESULT 4
US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
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QY 181 QLIDWMEADKVAAGPLIRSLAPAGWFIADKSGAGGSRGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDWMEADKVAAGPLIRSLAPAGWFIADKSGAGGSRGIIAALGPDGKPSRIVIYTTG 263
QY 241 SQATWDERNRQIAEIGASLIKHW 263
DB 264 SQATWDERNRQIAEIGASLIKHW 286

RESULT 7
US-09-025-769B-362
; Sequence 362, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moreney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-362

Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 7,1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDINSGEILSEFSRSEFPFMMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGRVGYIELDINSGEILSEFSRSEFPFMMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRIHYSDNDLVEYSPTEKHLTDGMTVRELCSAATMSDNTANILLTTIGGP 120
DB 84 AGQEQIGRIHYSDNDLVEYSPTEKHLTDGMTVRELCSAATMSDNTANILLTTIGGP 143
QY 121 KELITFLLHMGDHTVRLDRMEPELNEALPNDERDITTPVAMATTIKLITGELLTLASRQ 180
DB 144 KELITFLLHMGDHTVRLDRMEPELNEALPNDERDITTPVAMATTIKLITGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLIRSLAPAGWFIADKSGAGGSRGIIAALGPDGKPSRIVIYTTG 240

DB 204 QLIDWMEADKVAAGPLIRSLAPAGWFIADKSGAGGSRGIIAALGPDGKPSRIVIYTTG 263
QY 241 SQATWDERNRQIAEIGASLIKHW 263
DB 264 SQATWDERNRQIAEIGASLIKHW 286

RESULT 8
US-09-919-901-7
; Sequence 7, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/129,901
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
; US-09-919-901-7

Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 7,1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDINSGEILSEFSRSEFPFMMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGRVGYIELDINSGEILSEFSRSEFPFMMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRIHYSDNDLVEYSPTEKHLTDGMTVRELCSAATMSDNTANILLTTIGGP 120
DB 84 AGQEQIGRIHYSDNDLVEYSPTEKHLTDGMTVRELCSAATMSDNTANILLTTIGGP 143
QY 121 KELITFLLHMGDHTVRLDRMEPELNEALPNDERDITTPVAMATTIKLITGELLTLASRQ 180
DB 144 KELITFLLHMGDHTVRLDRMEPELNEALPNDERDITTPVAMATTIKLITGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLIRSLAPAGWFIADKSGAGGSRGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDWMEADKVAAGPLIRSLAPAGWFIADKSGAGGSRGIIAALGPDGKPSRIVIYTTG 263
QY 241 SQATWDERNRQIAEIGASLIKHW 263
DB 264 SQATWDERNRQIAEIGASLIKHW 286

RESULT 9
US-09-919-901-14
; Sequence 14, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02

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1 PRIOR APPLICATION NUMBER: 09/1263, 9933
2 PRIOR FILING DATE: 1999-02-08
3 PRIOR APPLICATION NUMBER: 09/1125, 6111
4 PRIOR FILING DATE: 1998-08-05
5 NUMBER OF SEQ ID NOS: 33
6 SOFTWARE: PatentIn Ver. 2.0
7 SEQ ID NO 14
8 LENGTH: 286
9 TYPE: PRT
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 OTHER INFORMATION: :
13 US-09-919-901-14

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Query Match	98.9%	Score 1330	DB 4	Length 286
Best Local Similarity	98.9%	Pred. No. 7.1e-139		
Matches 260	Conservative 1	Mismatches 2	Indels 0	Gaps 0

QY	HEPTLVKVDAAEQLGARVGYIELDINSSEILIESFRSEERPEPMSTFKVLLCGAVLSRID	60
Db	HEPTLVKVDAAEQLGARVGYIELDINSKILIESFRPERPEPMSTFKVLLCGAVLSRID	83
QY	AGGEOLGRRINHSQNDLVESPVTEKHLLTDGMTVELCSAITSMDNTAANLLITTTGGP	120
Db	AGGEOLGRRINHSQNDLVESPVTEKHLLTDGMTVELCSAITSMDNTAANLLITTTGGP	143
QY	KEITLAFIHHNGDHVTELDLRMEPELNEAIPNDRSDITTPVAMATTLRKLTIGSEILLTASRQ	188
Db	KEITLAFIHHNGDHVTELDLRMEPELNEAIPNDRSDITTPVAMATTLRKLTIGSEILLTASRQ	203
QY	QLIDNMEADKVAQPLLRSAIPAGWFIADKSGAGERGSGIIAALGPDGKPSRIIVITYTG	240
Db	QLIDNMEADKVAQPLLRSAIPAGWFIADKSGAGERGSGIIAALGPDGKPSRIIVITYTG	263
QY	SOATMDERNQIAETASLTIKHEM	263
Db	SOATMDERNQIAETASLTIKHEM	286

```

RESULT 10
US-09-919-901-21
: Sequence 21, Application US/09919901
: Patent No. 6599738
: GENERAL INFORMATION:
: APPLICANT: Potts, Karen E.
: APPLICANT: Jackson, Roberta L.
: APPLICANT: Patrick, Amy K.
: TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
: TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
: FILE REFERENCE: 0125-0005A
: CURRENT APPLICATION NUMBER: US/09/919,901
: CURRENT FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 09/262,933
: PRIOR FILING DATE: 1999-02-08
: PRIOR APPLICATION NUMBER: 09/129,611
: PRIOR FILING DATE: 1998-08-05
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 286
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: :
US-09-919-901-21

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	Query Match	Similarity	Score	DB	Length
Best Local	98.9%	98.9%	Pred. No. 7.1e-139		286
Matches	260	Conservative	1	Mismatches	2
				Indels	0
				Gaps	0
Ox	1	HPETLVKCKADDCGARGVGIETDLSNGEIIIESRSEBEPFMSTFYLLCGAVLSRID			60
Ob	24	HPETLVKCKADDCGARGVGIETDLSNGKLIIESRPEEPFMSTFYLLCGAVLSRID			83

Qy	6	AGGEOLGRRRIHNSONDIVYSPVTEKHLTDGATVRELCSAIIMSDMTAANLLTTTGGP	120
Db	84	AGGEOLGRRRIHNSONDIVYSPVTEKHLTDGATVRELCSAIIMSDMTAANLLTTTGGP	143
Qy	121	KELTALFANMGDHVRLDRWEPELNEAIPNDRDTTTPVAMATTLRKLLTGELLTLASRQ	180
Db	144	KELTALFANMGDHVRLDRWEPELNEAIPNDRDTTPVAMATTLRKLLTGELLTLASRQ	203
Qy	181	QLIDWMEADKVAGPLLRSLAPAGMTIADKSGAGEGSGGIIIAALGPDGKPSRIIVYITTG	240
Db	204	QLIDWMEADKVAGPLLRSLAPAGMTIADKSGAGEGSGGIIIAALGPDGKPSRIIVYITTG	263
Qy	241	SOATMDERNROIAETGASLITKHM	263
Db	264	SOATMDERNROIAETGASLITKHM	286

RESULT 11
 US-09-025-769B-285
 : Sequence 285 Application US/09025769B
 : Patent No. 630084
 : GENERAL INFORMATION:
 : APPLICANT: Knappik, Achim
 : APPLICANT: Knappik, Achim
 : APPLICANT: pack, Peter
 : APPLICANT: Ilag, Vic
 : APPLICANT: Ge, Liming
 : APPLICANT: Moroney, Simon
 : APPLICANT: Plueckthun, Andreas
 : TITLE OF INVENTION: Protein/(poly)peptide libraries
 : NUMBER OF SEQUENCES: 373
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 : STREET: 1251 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10021
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/025,769B
 : FILING DATE: 18-FEB-1998
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 95 11 3021.0
 : FILING DATE: 18-AUG-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: James F. Haley, Jr., Esq.
 : REGISTRATION NUMBER: 27,794
 : REFERENCE/DOCKET NUMBER: MORPHO/5
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212)596-9000
 : TELEFAX: (212)596-9090
 : INFORMATION FOR SEQ ID NO: 285:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 299 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-09-025-769B-285

Query Match	98.9%	Score 13.70	DB 4	length 299
Best Local Similarity	98.9%	Pred. 13.76-13.9		
Matches	260	Conservative 1	Mismatches 2	Indels 0
			Gaps	0
QY	1	HPETLVKKAEDDTGARVGIETIDINSGETIEFRSRERPRMSTPTVLICGAVLSID		60
Db	24	HPETLVKKAEDDTGARVGIETIDINSGETIEFRSRERPRMSTPTVLICGAVLSID		83
QY	61	AGQGLGRRIHYSQNDLVEYSPTVEKHLTDMTRELCSAAITMSDNTANLLITTTGGP		120

Db 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLLDGTVELCSAALTMSDNTAANLLTTIGSP 143
QY 121 KELTAFINMGDHVTRLDKRWEPBELNEAIPNDRDRTTTPVAMATTIRKLLTGELLTLASRQ 180
Db 144 KELTAFINMGDHVTRLDKRWEPBELNEAIPNDRDRTTTPVAMATTIRKLLTGELLTLASRQ 203
QY 181 QLIIDMWEADKXVAGPILRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTTG 240
Db 204 QLIIDMWEADKXVAGPILRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTTG 263
QY 241 SQATMDERNRQIAETGASLIRKM 263
Db 264 SQATMDERNRQIAETGASLIRKM 286

RESULT 12
US-09-025-769B-298
Sequence 298, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOREPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 298:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-298

Query Match 98.9%; Score 1330; DB 4; Length 299;
Best Local Similarity 98.9%; Pred. No. 7.6e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVAKYKADBDQIGARVGYIELDNGETLESFRSRRFPWMTFFKYLICGAVLSRID 60
Db 24 HPEITVAKYKADBDQIGARVGYIELDNGETLESFRSRRFPWMTFFKYLICGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLLDGTVELCSAALTMSDNTAANLLTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLLDGTVELCSAALTMSDNTAANLLTTIGSP 143

QY 121 KELTAFINMGDHVTRLDKRWEPBELNEAIPNDRDRTTTPVAMATTIRKLLTGELLTLASRQ 180
Db 144 KELTAFINMGDHVTRLDKRWEPBELNEAIPNDRDRTTTPVAMATTIRKLLTGELLTLASRQ 203
QY 181 QLIIDMWEADKXVAGPILRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTTG 240
Db 204 QLIIDMWEADKXVAGPILRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTTG 263
QY 241 SQATMDERNRQIAETGASLIRKM 263
Db 264 SQATMDERNRQIAETGASLIRKM 286

RESULT 13
US-09-025-769B-300
Sequence 300, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOREPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-300

Query Match 98.9%; Score 1330; DB 4; Length 299;
Best Local Similarity 98.9%; Pred. No. 7.6e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVAKYKADBDQIGARVGYIELDNGETLESFRSRRFPWMTFFKYLICGAVLSRID 60
Db 24 HPEITVAKYKADBDQIGARVGYIELDNGETLESFRSRRFPWMTFFKYLICGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLLDGTVELCSAALTMSDNTAANLLTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLLDGTVELCSAALTMSDNTAANLLTTIGSP 143
QY 121 KELTAFINMGDHVTRLDKRWEPBELNEAIPNDRDRTTTPVAMATTIRKLLTGELLTLASRQ 180


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Db      144  KELTAFHNMGDHYTRLDREMEPELNEAIPNDERDTTVPVAMATTLRKLTGELLTLASRQ 203
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Db      204  QLDIMWEADKVAGPLLSALPAGWFIADKSGAGERSGRTIITAAIGPDGKPSRIIVITYTG 263
QY      241  SQATMDERNRQIAETIGASLIKHW 263
Db      264  SQATMDERNRQIAETIGASLIKHW 286

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RESULT 14

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US-09-263-933-2
; Sequence 2, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; EARLIER FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-2

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Query Match      98.9%; Score 1330; DB 3; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.8e-137;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      61  AGGEOIGRRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGP 120
Db      2105 AGGEOIGRRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGP 2164
QY      121 KELTAFHNMGDHYTRLDREMEPELNEAIPNDERDTTVPVAMATTLRKLTGELLTLASRQ 180
Db      2165 KELTAFHNMGDHYTRLDREMEPELNEAIPNDERDTTVPVAMATTLRKLTGELLTLASRQ 2224
QY      181 QLDIMWEADKVAGPLLSALPAGWFIADKSGAGERSGRTIITAAIGPDGKPSRIIVITYTG 240
Db      2225 QLDIMWEADKVAGPLLSALPAGWFIADKSGAGERSGRTIITAAIGPDGKPSRIIVITYTG 2284
QY      241 SQATMDERNRQIAETIGASLIKHW 263
Db      2285 SQATMDERNRQIAETIGASLIKHW 2307

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RESULT 15
US-09-263-933-9
; Sequence 9, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08

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; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-9

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Query Match      98.9%; Score 1330; DB 3; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.8e-137;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      1  HPEITLVKVDADQDQAGRVYIELDINSGEILSFRESEFPMMSTFKVILCGAVLSRID 60
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QY      61  AGGEOIGRRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGP 120
Db      2105 AGGEOIGRRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATMSDNTAANLLTTTIGP 2164
QY      121 KELTAFHNMGDHYTRLDREMEPELNEAIPNDERDTTVPVAMATTLRKLTGELLTLASRQ 180
Db      2165 KELTAFHNMGDHYTRLDREMEPELNEAIPNDERDTTVPVAMATTLRKLTGELLTLASRQ 2224
QY      181 QLDIMWEADKVAGPLLSALPAGWFIADKSGAGERSGRTIITAAIGPDGKPSRIIVITYTG 240
Db      2225 QLDIMWEADKVAGPLLSALPAGWFIADKSGAGERSGRTIITAAIGPDGKPSRIIVITYTG 2284
QY      241 SQATMDERNRQIAETIGASLIKHW 263
Db      2285 SQATMDERNRQIAETIGASLIKHW 2307

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Search completed: June 18, 2004, 19:10:35
Job time : 23 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:01:08 ; Search time 45 Seconds

(without alignments)
1844.029 Million cell updates/sec

Title: EPPER526106.PEP
Perfect score: 1345
Sequence: 1 hpetlYkvKaaedqlgary.....tmdermqiaaeislkhw 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOCT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1330	98.9	286	Q00626	000626 staphylococ
2	1330	98.9	286	Q38058	Q38058 bacterioph
3	1327	98.7	286	Q8KQ72	Q8KQ72 escherichia
4	1325	98.5	286	Q9R748	Q9R748 klebsiella
5	1322	98.3	286	Q8KSD2	Q8KSD2 escherichia
6	1322	98.3	286	Q34176	Q34176 klebsiella
7	1321	98.2	286	Q9JAC0	Q9JAC0 proteus mir
8	1321	98.2	286	Q9JAB0	Q9JAB0 escherichia
9	1321	98.2	286	Q9AGJ5	Q9AGJ5 escherichia
10	1321	98.2	286	Q9R435	Q9R435 klebsiella
11	1321	98.2	286	Q9RMS2	Q9RMS2 escherichia
12	1321	98.2	286	Q8KMX4	Q8KMX4 escherichia
13	1321	98.2	286	Q8KND8	Q8KND8 klebsiella
14	1321	98.2	286	Q9RNM4	Q9RNM4 escherichia
15	1321	98.2	286	Q93372	Q93372 capnocytoph
16	1321	98.2	286	Q932Y6	Q932Y6 pseudomonas

17	1320	98.1	286	Q9R745	Q9R745 escherichia
18	1320	98.1	286	Q8KRH0	Q8KRH0 klebsiella
19	1320	98.1	286	Q93A77	Q93A77 escherichia
20	1319	98.1	286	Q9S678	Q9S678 klebsiella
21	1319	98.1	286	Q9FAA2	Q9FAA2 escherichia
22	1319	98.1	286	Q8VP43	Q8VP43 klebsiella
23	1319	98.1	286	Q48406	Q48406 klebsiella
24	1319	98.1	286	Q8GA85	Q8GA85 escherichia
25	1319	98.1	286	Q844X1	Q844X1 klebsiella
26	1318	98.0	286	Q9AFC8	Q9AFC8 escherichia
27	1318	98.0	286	Q9S679	Q9S679 escherichia
28	1318	98.0	286	Q8L1Y1	Q8L1Y1 escherichia
29	1318	98.0	286	F78144	F78144 escherichia
30	1318	98.0	286	Q9RMS4	Q9RMS4 escherichia
31	1318	98.0	286	Q91UY8	Q91UY8 pseudomonas
32	1318	98.0	286	Q9EYX1	Q9EYX1 escherichia
33	1317	97.9	263	Q9R2G5	Q9R2G5 escherichia
34	1317	97.9	286	Q93A79	Q93A79 escherichia
35	1317	97.9	286	Q9R429	Q9R429 morangella
36	1317	97.9	286	Q937U3	Q937U3 escherichia
37	1316	97.8	286	Q8KQ59	Q8KQ59 klebsiella
38	1316	97.8	286	Q8RPY9	Q8RPY9 enterobacte
39	1316	97.8	286	Q9R312	Q9R312 proteus mir
40	1316	97.8	286	Q46354	Q46354 escherichia
41	1315	97.8	286	Q936T3	Q936T3 klebsiella
42	1315	97.8	286	Q8KMX3	Q8KMX3 escherichia
43	1315	97.8	286	Q9ZFW9	Q9ZFW9 morangella
44	1314	97.7	286	Q933Z8	Q933Z8 escherichia
45	1314	97.7	286	Q9AEY6	Q9AEY6 klebsiella

ALIGNMENTS

RESULT 1
000626 PRELIMINARY: PRT; 286 AA.
AC 000626; Q57339; Q08022; Q08102; Q09490; Q09463; Q09393; Q09396;
AC 009397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;
AC 009405; Q09406; Q09407; Q09408; Q09481; Q09482;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).
GN Bla OR AMP.
OS Staphylococcus aureus,
OS Escherichia coli,
OS unidentified, and
OS Alcaligenes hydrophillus.
OG Plasmid pUD84, plasmid pRP4 and plasmid pRAY-1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 562, 32644, 516;
RN [1]
RP SEQUENCE FROM N.A.
RA Lieberman B.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Needham C., Noble W.C., Dyke K.G.H.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Kovach M.E.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K11;
RX MEDLINE=97074643; PubMed=8917070;
RA Seretbrjstki I.G., Vassil V.M., Tsygankov Y.D.;

"Two new members of the bio B superfamily: cloning, sequencing and expression of bio B genes of *Methylobacillus flagellatum* and *Corynebacterium glutamicum*.";
 RT Gene 175:15-22(1996).
 RL [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L., Little M., Breilung F.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9636236; PubMed=8770413;
 RA Rees S., Coote J., Stables J., Goodson S., Harris S., Lee M.G.;
 RT "Bicistronic vector for the creation of stable mammalian cell lines that predisposes all antibiotic-resistant cells to express recombinant protein.";
 RL Biotechniques 20:102-104(1996).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Lou Y., Holtz A.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97105907; PubMed=8948655;
 RA Storch T., Kneth U., Kolhakar R., Sprengel R., Seeburg P.H.;
 RT "Rapid construction in yeast of complex targeting vectors for gene manipulation in the mouse.";
 RL Nucleic Acids Res. 24:4594-4596(1996).
 RN [10]
 RP SEQUENCE FROM N.A.
 RA Lu Q.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RA Holtz A., Lou Y.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92302280; PubMed=1319065;
 RA Gossen M., Bujard H.;
 RT "Tight control of gene expression in mammalian cells by tetracycline-responsive promoters.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551(1992).
 RN [13]
 RP SEQUENCE FROM N.A.
 RA Gossen M., Bujard H.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RA Holtz A., Lou Y.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96032859; PubMed=7567477;
 RA Baron U., Freundlieb S., Gossen M., Bujard H.;
 RT "Co-regulation of two gene activities by tetracycline via a bidirectional promoter.";
 RL Nucleic Acids Res. 23:3605-3606(1995).
 RN [16]
 RP SEQUENCE FROM N.A.
 RA Baron U., Freundlieb S., Gossen M., Bujard H.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [17]
 RP SEQUENCE FROM N.A.
 RA Kites P.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [18]
 RP SEQUENCE FROM N.A.
 RA Schlieper D., von Wilcken-Bergmann B., Schmidt M., Sobek H., Mueller-Hill B.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-

CC AMINO ACID.
 CC -1- SIMILARITY: THIS IS A CLASS-A BETA-LACTAMASE.
 DR EMBL: U36912; AAB39957.1; -;
 DR EMBL: M74750; AAA24057.1; -;
 DR EMBL: U36911; AAB39956.1; -;
 DR EMBL: U31280; AAC44581.1; -;
 DR EMBL: Y12694; CAA73226.1; -;
 DR EMBL: U63018; AAC53676.1; -;
 DR EMBL: U86815; AAB91427.1; -;
 DR EMBL: U89827; AAB64384.1; -;
 DR EMBL: U89829; AAB64387.1; -;
 DR EMBL: U89830; AAB64389.1; -;
 DR EMBL: A24782; CAA01735.1; -;
 DR EMBL: U89931; AAB64391.1; -;
 DR EMBL: U89672; AAB49980.1; -;
 DR EMBL: AJ001614; CAA04868.1; -;
 DR EMBL: U89932; AAB64392.1; -;
 DR EMBL: U89933; AAB64394.1; -;
 DR EMBL: U89934; AAB64395.1; -;
 DR EMBL: U89935; AAB64398.1; -;
 DR EMBL: U89937; AAB64401.1; -;
 DR EMBL: U89938; AAB64403.1; -;
 DR EMBL: U89939; AAB64405.1; -;
 DR EMBL: U89940; AAB64407.1; -;
 DR EMBL: U89671; AAB49977.1; -;
 DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO: GO:0008800; F:beta-lactamase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0046577; P:response to antibiotic; IEA.
 DR InterPro: IPR001466; Beta_lactamase.
 DR InterPro: IPR000871; Beta_lactamase_A.
 DR Pfam: PF00144; beta_lactamase; 1.
 DR PRINTS: PR00118; BLACTAMASEA.
 DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
 KM Antibiotic resistance; Hydrolase; Plasmid; Signal.
 FT SIGNAL
 FT CHAIN 1 23
 FT SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 SQ
 Query Match 98.9%; Score 1330; DB 2; Length 286;
 Best Local Similarity 98.9%; Pred. No. 4.3e-104;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HPEITLVKVKDAEDQAGAVGVYIELDLNSGEILIESFRSRRPFWMTFKYLICGAVLSRD 60
 DB 24 HPEITLVKVKDAEDQAGAVGVYIELDLNSGEILIESFRSRRPFWMTFKYLICGAVLSRD 83
 QY 61 AGQEQIGRIHYSQNDLVEYSPYTERKHLTDGWTRELCSAATMSDNTFANLLTTIGSP 120
 DB 84 AGQEQIGRIHYSQNDLVEYSPYTERKHLTDGWTRELCSAATMSDNTFANLLTTIGSP 143
 QY 121 KELTAFILNMGDHYVRLDRWEPELNEAIPNDRDITTPYAMAATTIRKLLTGELLTASRQ 180
 DB 144 KELTAFILNMGDHYVRLDRWEPELNEAIPNDRDITTPYAMAATTIRKLLTGELLTASRQ 203
 QY 181 QLIIDWEADKVAQPLIRSLPAQMTIADPSGAGGERSRGIITAAIPDQEPSRIIVYITG 240
 DB 204 QLIIDWEADKVAQPLIRSLPAQMTIADPSGAGGERSRGIITAAIPDQEPSRIIVYITG 263
 QY 241 SQATMDERNROIAETGASLIKHW 263
 DB 264 SQATMDERNROIAETGASLIKHW 286
 RESULT 2
 ID Q38058 PRELIMINARY; PRT; 286 AA.
 AC Q38058;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-JUN-2003 (T-EMblrel. 24, last annotation update)
 DE Beta lactamase.
 GN BIA.

OS Bacteriophage phi-X174.
 OC Viruses; ssDNA viruses; Microviridae; Microvirus.
 ON NCBI_TaxID=10847;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=95172401; PubMed=7867948;
 RT Heinrich B., Schindlberger B.;
 RT "A variant of phiX174 gene E-based positive selection vectors with
 RT enhanced lytic potential.";
 RL Gene 154:51-54(1995).
 DR EMBL; Z35638; CA84692.1; -
 DR PIR; S47061; S47061.
 DR HSP; P00810; 1BLT.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase.
 DR Pfam; PF00144; beta-lactamase_1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31557 MM; SEB2F275375FA9 CRC64;

Query Match 98.9%; Score 1330; DB 9; Length 286;
 Best Local Similarity 98.9%; Pred. No. 4.3e-104;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVYIELDNSGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVDADQOLGARVYIELDNSGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGEOUGRRIRHYSQNDLVKXSPVTEKRLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGGEOUGRRIRHYSQNDLVKXSPVTEKRLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILHMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTLKLTGELLTLASRQ 180
 DB 144 KEITAFILHMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTLKLTGELLTLASRQ 203
 QY 181 QLDIMNEADKVAPELRSALPAGMFLADKSGAGERSRGITAAIGPDGKPSRIVITYTG 240
 DB 204 QLDIMNEADKVAPELRSALPAGMFLADKSGAGERSRGITAAIGPDGKPSRIVITYTG 263
 QY 241 SQATMDERNRQIAEIGASLIKHW 263
 DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 3
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 AC Q8KQ72;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, last sequence update)
 DT 01-UN-2003 (T-EMBLrel. 24, last annotation update)
 DE Class A beta-lactamase TEM-106.
 GN BLATM-106.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 ON NCBI_TaxID=962;
 RP SEQUENCE FROM N.A.
 RC STRAIN=YMC9/12/74;
 RA Yum J.H., Yong D., Shin J.H., Lee K., Chong Y.;
 RT "Characterization of a new extended-spectrum beta-lactamase (TEM-106)
 RT in an Escherichia coli clinical isolate in Korea.";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBD databases.
 DR EMBL; AY101578; AAM52207.1; -
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase.
 DR Pfam; PF00144; beta_lactamase_1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31484 MM; 137161BA6E9AFB6 CRC64;

Query Match 98.7%; Score 1327; DB 2; Length 286;
 Best Local Similarity 98.1%; Pred. No. 7.8e-104;
 Matches 258; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVYIELDNSGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVDADQOLGARVYIELDNSGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGEOUGRRIRHYSQNDLVKXSPVTEKRLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGGEOUGRRIRHYSQNDLVKXSPVTEKRLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILHMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTLKLTGELLTLASRQ 180
 DB 144 KEITAFILHMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTLKLTGELLTLASRQ 203
 QY 181 QLDIMNEADKVAPELRSALPAGMFLADKSGAGERSRGITAAIGPDGKPSRIVITYTG 240
 DB 204 QLDIMNEADKVAPELRSALPAGMFLADKSGAGERSRGITAAIGPDGKPSRIVITYTG 263
 QY 241 SQATMDERNRQIAEIGASLIKHW 263
 DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 4
 Q9RT48 PRELIMINARY; PRT; 286 AA.
 AC Q9RT48;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
 DT 01-MAY-2002 (T-EMBLrel. 20, last annotation update)
 DE Beta-lactamase class A (Fragment).
 GN BLATM-20.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 ON NCBI_TaxID=573;
 RP SEQUENCE FROM N.A.
 RC STRAIN=A268;
 RX MEDLINE=99216918; PubMed=10103213;
 RA Arlet G., Goussard S., Courvalin P., Philippot A.;
 RT "Sequence of the genes for TEM-20, TEM-21, TEM-22 and TEM-29 extended-
 RT spectrum beta-lactamases.";
 RL Antimicrob. Agents Chemother. 43:969-971(1999).
 DR EMBL; Y17581; CAA76793.1; -
 DR HSP; P00810; 1TEM.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase.
 DR Pfam; PF00144; beta-lactamase_1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON TER 286
 SQ SEQUENCE 286 AA; 31515 MM; 155F7CE493A16FB8 CRC64;

Query Match 98.5%; Score 1325; DB 2; Length 286;
 Best Local Similarity 98.1%; Pred. No. 1.1e-103;
 Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVYIELDNSGEILSFSEERFPMMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVDADQOLGARVYIELDNSGEILSFSEERFPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGEOUGRRIRHYSQNDLVKXSPVTEKRLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGGEOUGRRIRHYSQNDLVKXSPVTEKRLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILHMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTLKLTGELLTLASRQ 180
 DB 144 KEITAFILHMGDHTVRLDRWEPELNEAIPNDRDITTPVAMATTLKLTGELLTLASRQ 203
 QY 181 QLDIMNEADKVAPELRSALPAGMFLADKSGAGERSRGITAAIGPDGKPSRIVITYTG 240

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Db      204 QIIMWEADKXAGPLIRSLPAGMFIADKSGASRGSGIIAALGDPKPSRIVIYTTG 263
Qy      241 SOATMDERNROIAETGASLTKHW 263
Db      264 SOATMDERNROIAETGASLTKHW 286

RESULT 5
Q8KSD2 ID Q8KSD2 PRELIMINARY; PRT; 286 AA.
AC Q8KSD2;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Beta-lactamase TEM-105.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y.-B., Li X., Yu Y.-S.;
RT "Cloning and promiscuous expression of the encoding gene of TEM-105
RT type of beta-lactamases."
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF516720; AAC61953.1; -.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31542 MW; B3DE92C996C5A5EC CRC64;

Query Match 98.3%; Score 1322; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.1e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HPEITVKYKADBDQAGRVGYIELDNGEILSFSESERPMSFTFYLLCGAVLSRD 60
Db 24 HPEITVKYKADBDQAGRVGYIELDNGEILSFSESERPMSFTFYLLCGAVLSRD 83
Qy 61 AGQQLGRRIHYSQNDLVKYSPTVEKHLTDGNTVELCSAATMSDNTAAILTTTGGP 120
Db 84 AGQQLGRRIHYSQNDLVKYSPTVEKHLTDGNTVELCSAATMSDNTAAILTTTGGP 143
Qy 121 KELLTFLNMGDHVTRLDRWPELNEALPNDERDITTPVAAATTLRKLLTGELITLASRQ 180
Db 144 KELLTFLNMGDHVTRLDRWPELNEALPNDERDITTPVAAATTLRKLLTGELITLASRQ 203
Qy 181 QIIMWEADKXAGPLIRSLPAGMFIADKSGASRGSGIIAALGDPKPSRIVIYTTG 240
Db 204 QIIMWEADKXAGPLIRSLPAGMFIADKSGASRGSGIIAALGDPKPSRIVIYTTG 263
Qy 241 SOATMDERNROIAETGASLTKHW 263
Db 264 SOATMDERNROIAETGASLTKHW 286

RESULT 6
Q34176 ID Q34176 PRELIMINARY; PRT; 286 AA.
AC Q34176;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Beta-lactamase TEM-43.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]

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RP SEQUENCE OF 1-286 FROM N.A.
RX MEDLINE=96325432; Pubmed=9661002;
RA Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahn D.F., Bush K.;
RT "Ceftazidime-resistant Klebsiella pneumoniae and Escherichia coli
RT isolates producing TEM-10 and TEM-43 beta-lactamases from St. Louis,
RT Missouri."
RL Antimicrob. Agents Chemother. 42:1671-1676(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahn D.F., Bush K.;
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; U95363; AAC32899.2; -.
DR HSSP; P00810; ITEM.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31465 MW; 1371745A6119B5B6 CRC64;

Query Match 98.3%; Score 1322; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.1e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 HPEITVKYKADBDQAGRVGYIELDNGEILSFSESERPMSFTFYLLCGAVLSRD 60
Db 24 HPEITVKYKADBDQAGRVGYIELDNGEILSFSESERPMSFTFYLLCGAVLSRD 83
Qy 61 AGQQLGRRIHYSQNDLVKYSPTVEKHLTDGNTVELCSAATMSDNTAAILTTTGGP 120
Db 84 AGQQLGRRIHYSQNDLVKYSPTVEKHLTDGNTVELCSAATMSDNTAAILTTTGGP 143
Qy 121 KELLTFLNMGDHVTRLDRWPELNEALPNDERDITTPVAAATTLRKLLTGELITLASRQ 180
Db 144 KELLTFLNMGDHVTRLDRWPELNEALPNDERDITTPVAAATTLRKLLTGELITLASRQ 203
Qy 181 QIIMWEADKXAGPLIRSLPAGMFIADKSGASRGSGIIAALGDPKPSRIVIYTTG 240
Db 204 QIIMWEADKXAGPLIRSLPAGMFIADKSGASRGSGIIAALGDPKPSRIVIYTTG 263
Qy 241 SOATMDERNROIAETGASLTKHW 263
Db 264 SOATMDERNROIAETGASLTKHW 286

RESULT 7
Q91AC0 ID Q91AC0 PRELIMINARY; PRT; 286 AA.
AC Q91AC0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Class A beta-lactamase.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferilli M., Amicosante G.;
RT "A new TEM ESBu highly active against cefotaxime in Proteus mirabilis
RT clinical isolate."
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF143804; AAF66553.1; -.
DR HSSP; P00810; ITEM.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31514 MW; 8B437C51FC5D60A8 CRC64;

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Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQOLGARVGYIELDINSGETLSEFSEERFPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQOLGARVGYIELDINSGETLSEFSEERFPMSSTFKVLLCGAVLSRID 83

QY 61 AGGOLGRRIHYSQNDLVKSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGGOLGRRIHYSQNDLVKSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143

QY 121 KELTAFIANNMGDHTVRLDMEPELNEAIPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 180
DB 144 KELTAFIANNMGDHTVRLDMEPELNEAIPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203

QY 181 QLDIMWEADKVAGPLRSALPAGWFIADKSGAGERSGRTIIAALGPDGKRSRIVVIYTTG 240
DB 204 QLDIMWEADKVAGPLRSALPAGWFIADKSGAGERSGRTIIAALGPDGKRSRIVVIYTTG 263

QY 241 SOATMDERNROIAEIGASLTKHW 263
DB 264 SOATMDERNROIAEIGASLTKHW 286

RESULT 8
Q93A80 PRELIMINARY; PRT; 286 AA.
AC Q93A80; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Inhibitor-resistant beta-lactamase TEM-81.
GN BLATEM-81.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20448741; Pubmed=10991849;
RA Ieflon-Guibout V., Speeldooren V., Heym B., Nicolas-Chanoine M.;
RT "Epidemiological survey of amoxicillin-clavulanate resistance and
corresponding molecular mechanisms in Escherichia coli isolates in
France: new genetic features of bla(TEM) gene";
RU Antimicrob. Agents Chemother. 44:2709-2714(2000).
[2]
RP SEQUENCE FROM N.A.
RA Ieflon-Guibout V., Speeldooren V., Heym B., Nicolas-Chanoine M.-H.;
RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF427127; AAL29433.1; -;
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31483 MW; 582B34DDA06818F8 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.3%; Pred. No. 2.5e-103;
Matches 256; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQOLGARVGYIELDINSGETLSEFSEERFPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQOLGARVGYIELDINSGETLSEFSEERFPMSSTFKVLLCGAVLSRID 83

QY 61 AGGOLGRRIHYSQNDLVKSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGGOLGRRIHYSQNDLVKSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143

QY 121 KELTAFIANNMGDHTVRLDMEPELNEAIPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 180
DB 144 KELTAFIANNMGDHTVRLDMEPELNEAIPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203

QY 181 QLDIMWEADKVAGPLRSALPAGWFIADKSGAGERSGRTIIAALGPDGKRSRIVVIYTTG 240
DB 204 QLDIMWEADKVAGPLRSALPAGWFIADKSGAGERSGRTIIAALGPDGKRSRIVVIYTTG 263

QY 241 SOATMDERNROIAEIGASLTKHW 263
DB 264 SOATMDERNROIAEIGASLTKHW 286

RESULT 9
Q9AGJ5 PRELIMINARY; PRT; 286 AA.
AC Q9AGJ5; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Extended spectrum beta-lactamase TEM-63.
GN BLATEM-63.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanson N.D., Moïand E.S., Pitout J.D.;
RT "TEM-63, A Novel TEM-type Extended Spectrum Beta-lactamase Expressed
In Three Different Genera of Enterobacteriaceae, from South Africa";
RU Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF332513; AAK17194.1; -;
DR HSSP: P00810; ITEM.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; beta-lactamase; 1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31449 MW; AEBB60086CE3AEB3 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQOLGARVGYIELDINSGETLSEFSEERFPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQOLGARVGYIELDINSGETLSEFSEERFPMSSTFKVLLCGAVLSRID 83

QY 61 AGGOLGRRIHYSQNDLVKSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGGOLGRRIHYSQNDLVKSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143

QY 121 KELTAFIANNMGDHTVRLDMEPELNEAIPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 180
DB 144 KELTAFIANNMGDHTVRLDMEPELNEAIPNDERDTTTPVAMATTLTKLLTGELLTLASRQ 203

QY 181 QLDIMWEADKVAGPLRSALPAGWFIADKSGAGERSGRTIIAALGPDGKRSRIVVIYTTG 240
DB 204 QLDIMWEADKVAGPLRSALPAGWFIADKSGAGERSGRTIIAALGPDGKRSRIVVIYTTG 263

RESULT 10
Q9R435 PRELIMINARY; PRT; 286 AA.
AC Q9R435; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE EXTENDED SPECTRUM beta-lactamase.
GN BLATEM-52.
OS Klebsiella pneumoniae.

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OG Plasmid pK50-2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=KMK107;
RA Cho D.T., Shin H.S.;
RT "Molecular Evolution of blaTEM of Extended Spectrum of beta-lactamase
  (ESBL) in Klebsiella pneumoniae isolated in Korea.";
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=NEM865;
RA Poyart C., Magnier P., Quesnes G., Berche P., Trieu-Quot P.;
RT "A novel extended-spectrum TEM-type beta-lactamase from Klebsiella
  pneumoniae hydrolyzing Moxalactam.";
RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF027199; AAB84239.1; -.
DR EMBL; Y13612; CAA73933.1; -.
DR PDB; 1HTZ; 21-MAR-01.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BIACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31514 MW; 13717ACB58F6FB6 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 HPEITLVKVKDADQUGARVGYIELDNGEILLESFSEPRPMMSTFYKLLCGAVLSRD 60
DB HPEITLVKVKDADQUGARVGYIELDNGEILLESFSEPRPMMSTFYKLLCGAVLSRD 83
OY 61 AGQEQIGRIHYSQNDIVYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGGP 120
DB AGQEQIGRIHYSQNDIVYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGGP 143
OY 121 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 180
DB KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 203
OY 144 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 203
DB 144 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 203
OY 181 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 240
DB 181 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 240
OY 204 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 263
DB 204 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 263
OY 241 SQATMDERNROIAETGASLIKHM 263
DB 241 SQATMDERNROIAETGASLIKHM 263
OY 264 SQATMDERNROIAETGASLIKHM 286
DB 264 SQATMDERNROIAETGASLIKHM 286

RESULT 11
Q9RMS2 PRELIMINARY; PRT; 286 AA.
ID Q9RMS2;
AC Q9RMS2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Inhibitor-resistant beta-lactamase TEM-76.
GN BLATM-76.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20448741; PubMed=10991849;
RX Leffon-Guibout V., Speldooren V., Heym B., Nicolas-Chanoine M.-H.;
RT "Epidemiological survey of amoxicillin-clavulanate resistance and

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RT corresponding molecular mechanisms in Escherichia coli isolates in
  France: new genetic features of bla(TEM) genes.";
RL Antimicrob. Agents Chemother. 44:2709-2714(2000).
DR EMBL; AF190694; AAF05613.1; -.
DR HSSP; P00810; 1XPB.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BIACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31485 MW; 63BF483A7055BD7 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 HPEITLVKVKDADQUGARVGYIELDNGEILLESFSEPRPMMSTFYKLLCGAVLSRD 60
DB HPEITLVKVKDADQUGARVGYIELDNGEILLESFSEPRPMMSTFYKLLCGAVLSRD 83
OY 24 HPEITLVKVKDADQUGARVGYIELDNGEILLESFSEPRPMMSTFYKLLCGAVLSRD 83
DB 24 HPEITLVKVKDADQUGARVGYIELDNGEILLESFSEPRPMMSTFYKLLCGAVLSRD 83
OY 61 AGQEQIGRIHYSQNDIVYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGGP 120
DB AGQEQIGRIHYSQNDIVYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGGP 143
OY 84 AGQEQIGRIHYSQNDIVYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGGP 143
DB 84 AGQEQIGRIHYSQNDIVYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGGP 143
OY 121 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 180
DB 121 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 180
OY 144 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 203
DB 144 KELTAFHNMGDHVTDLRWEPELNEALPNDERDRTTPAAMATTIRKLLTGLTLTASRQ 203
OY 181 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 240
DB 181 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 240
OY 204 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 263
DB 204 QLTDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIIALGPDGKPSRIVIYTTG 263
OY 241 SQATMDERNROIAETGASLIKHM 263
DB 241 SQATMDERNROIAETGASLIKHM 263
OY 264 SQATMDERNROIAETGASLIKHM 286
DB 264 SQATMDERNROIAETGASLIKHM 286

RESULT 12
Q8KMX4 PRELIMINARY; PRT; 286 AA.
ID Q8KMX4;
AC Q8KMX4;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, last annotation update)
DE TEM-93 ES-beta-lactamase.
GN BLA-TEM-93.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CLSIS 3445/98;
RX Gniadkowski M.;
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=CLSIS 3445/98;
RX Baranik A.;
RT "Evolution of TEM extended-spectrum beta-lactamases in Poland.";
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ318093; CAC85660.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BIACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31514 MW; 1555DCB499016FB8 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;

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Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 1 HPEITLVKVDADQDQGVYIELDINSGEILSFSPSEFPFPMSTFKVILCGAVLSRID 60
DB 24 HPEITLVKVDADQDQGVYIELDINSGEILSFSPSEFPFPMSTFKVILCGAVLSRID 83
QY 61 AGOEOLGRRIRHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGOEOLGRRIRHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143
QY 121 KELTAFILHNMGDHVTLRDRWPEPELNEAIPNDRDPTTPVAMATTIRKLITGELLTLASRQ 180
DB 144 KELTAFILHNMGDHVTLRDRWPEPELNEAIPNDRDPTTPVAMATTIRKLITGELLTLASRQ 203
QY 181 QLIDMMEADKVAAGPLIRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDMMEADKVAAGPLIRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROIAGSLIKHW 263
DB 264 SOATMDERNROIAGSLIKHW 286

```

RESULT 13

Q8KSD3 PRELIMINARY; PRT; 286 AA.

ID AC O8KSD3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-UN-2003 (TrEMBLrel. 24, Last annotation update)
DB Beta-lactamase TEM-104.
OS Klebsiella pneumoniae.
OC Enterobacteriaceae; Klebsiella.
NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RA Li J.-B., Li X., Yu Y.-S.;
RT "Cloning and promiscuous expression of the encoding gene of TEM-104
RT type of beta-lactamases.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516719; AAM61952.1; -
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31543 MW; BB679BC8B18934B CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVDADQDQGVYIELDINSGEILSFSPSEFPFPMSTFKVILCGAVLSRID 60
DB 24 HPEITLVKVDADQDQGVYIELDINSGEILSFSPSEFPFPMSTFKVILCGAVLSRID 83
QY 61 AGOEOLGRRIRHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGOEOLGRRIRHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143
QY 121 KELTAFILHNMGDHVTLRDRWPEPELNEAIPNDRDPTTPVAMATTIRKLITGELLTLASRQ 180
DB 144 KELTAFILHNMGDHVTLRDRWPEPELNEAIPNDRDPTTPVAMATTIRKLITGELLTLASRQ 203
QY 181 QLIDMMEADKVAAGPLIRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDMMEADKVAAGPLIRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROIAGSLIKHW 263
DB 264 SOATMDERNROIAGSLIKHW 286

```

RESULT 14

```

Q9RN48 PRELIMINARY; PRT; 286 AA.
ID AC Q9RN48;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DB Beta-lactamase variant TEM-70.
GN BLATEM-70.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Egelstein M.V.;
RT "Sequence diversity of the genes encoding broad-spectrum TEM-type
RT beta-lactamases in clinical Escherichia coli strains."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF188199; AAF01046.1; -
DR HSSP; P00810; 1XPB.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT VARIANT 202
SQ SEQUENCE 286 AA; 31487 MW; E864BA43B9776BD9 CRC64;

```

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVDADQDQGVYIELDINSGEILSFSPSEFPFPMSTFKVILCGAVLSRID 60
DB 24 HPEITLVKVDADQDQGVYIELDINSGEILSFSPSEFPFPMSTFKVILCGAVLSRID 83
QY 61 AGOEOLGRRIRHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGOEOLGRRIRHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143
QY 121 KELTAFILHNMGDHVTLRDRWPEPELNEAIPNDRDPTTPVAMATTIRKLITGELLTLASRQ 180
DB 144 KELTAFILHNMGDHVTLRDRWPEPELNEAIPNDRDPTTPVAMATTIRKLITGELLTLASRQ 203
QY 181 QLIDMMEADKVAAGPLIRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 QLIDMMEADKVAAGPLIRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROIAGSLIKHW 263
DB 264 SOATMDERNROIAGSLIKHW 286

```

RESULT 15

```

O32372 PRELIMINARY; PRT; 286 AA.
ID AC O32372;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DB Beta-lactamase class A.
GN BLA TEM-17.
OS Capnocytophaga ochracea.
OC Bacteria; Bacteroidetes; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
NCBI_TaxID=1018;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20145403; PubMed=10681352;
```

RA Rosenau A., Cattier B., Goussset P., Harriau P., Philippon A.,
RA Quentin R.,
RT "Capnocytophaga ochracea: characterization of a plasmid-encoded
RT extended-spectrum TEM-17 beta-lactamase in the phylum Flavobacter-
RT Bacteroides";
RT Antimicrob. Agents Chemother. 44:760-762 (2000).
DR EMBL; Y14574; CAA74912.2; -.
DR HSSP; P00810; 1XPB.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31514 MW; BD498FB9D369345 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.5e-103;
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY	1	HPETLVKKAEDQLGARVGIIEIDLSNGELLESRSEPRFPMMSTFKVILCGAVLSRID	60
Db	24	HPETLVKKAEDQLGARVGIIEIDLSNGELLESRSEPRFPMMSTFKVILCGAVLSRID	83
QY	61	AGEQQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAAITMSDNTANILLTTGGP	120
Db	84	AGEQQLGRRIHYSQNDIVKSPVTEKHLTDGMTVRELCSAAITMSDNTANILLTTGGP	143
QY	121	KELTAPFLHNMGDHYTRLDWMEPELNEAIPNDEBDTTTPVAMATTIRKLLTGELLTASRQ	180
Db	144	KELTAPFLHNMGDHYTRLDWMEPELNEAIPNDEBDTTTPVAMATTIRKLLTGELLTASRQ	203
QY	181	QLIDWMDKVAQPIILRSALPAQWFIADKSGAGERSGRTIAALGPDGKPSRIVIYITTG	240
Db	204	QLIDWMDKVAQPIILRSALPAQWFIADKSGAGERSGRTIAALGPDGKPSRIVIYITTG	263
QY	241	SOATMDERNROIATETGASLIKHW	263
Db	264	SOATMDERNROIATETGASLIKHW	286

Search completed: June 18, 2004, 19:10:01
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:27:53 ; Search time 60 Seconds
(without alignments)
1238.500 Million cell updates/sec

Title: EPPER526106.PEP
Perfect score: 1345
Sequence: 1 hpecltkvkkaedqlgarv.....tmdermqiaegaslkhw 263

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesegp290a04:*
2: genesegp1980s:*
3: genesegp1990s:*
4: genesegp2000s:*
5: genesegp2001s:*
6: genesegp2002s:*
7: genesegp2003as:*
8: genesegp2003bs:*
9: genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1330	98.9	263 4 AAE05544	Aae05544 E. coli m
2	1330	98.9	263 4 AAB36692	Aab36692 Escherich
3	1330	98.9	264 2 AAW16634	Aaw16634 Beta-lact
4	1330	98.9	264 2 AAW18680	Aaw18680 Inticell
5	1330	98.9	286 2 AAR31575	Aar31575 Ampicilli
6	1330	98.9	286 2 AAR37619	Aar37619 Secretory
7	1330	98.9	286 2 AAR96423	Aar96423 Cytochrom
8	1330	98.9	286 2 AAW16635	Aaw16635 Beta-lact
9	1330	98.9	286 2 AAW18679	Aaw18679 Secretory
10	1330	98.9	286 2 AAY08529	Aay08529 Vector pA
11	1330	98.9	286 3 AAB10442	Aab10442 Expressio
12	1330	98.9	286 3 AAB10438	Aab10438 Expressio
13	1330	98.9	286 3 AAB10440	Aab10440 Expressio
14	1330	98.9	286 4 AAB50898	Aab50898 Protein e
15	1330	98.9	286 4 AAB31173	Aab31173 Amino aci
16	1330	98.9	286 5 AAW75551	Aaw75551 Amino aci
17	1330	98.9	286 6 AABP55474	Aabp55474 Vector pc
18	1330	98.9	286 6 ABR43622	Abri43622 Cloning v
19	1330	98.9	290 4 AAW23219	Aaw23219 Novel hum
20	1330	98.9	290 4 AAM84362	Aam84362 Human imm
21	1330	98.9	327 2 AAW16636	Aaw16636 Beta-lact
22	1330	98.9	327 2 AAW18681	Aaw18681 Membrane-
23	1330	98.9	408 6 ABR55981	Abri55981 hCG beta-
24	1330	98.9	585 6 ADA67747	Ada67747 Beta-lact
25	1330	98.9	1088 2 AAR88636	Aar88636 Plasmid p

26	1330	98.9	1277 2 AAR52701	Aar52701 Plasmid p
27	1330	98.9	2307 3 AAY70064	Aay70064 Recombina
28	1330	98.9	2307 3 AAY70066	Aay70066 Recombina
29	1329	98.8	286 2 AAY06551	Aay06551 Escherich
30	1329	98.8	1293 7 ADC22811	Adc22811 Human G p
31	1329	98.8	1967 6 ABB82793	Abb82793 Amino aci
32	1325	98.5	265 2 AAY08234	Aay08234 E. coli R
33	1325	98.5	265 2 AAY08232	Aay08232 E. coli R
34	1325	98.5	265 2 AAW48613	Aaw48613 Escherich
35	1325	98.5	265 2 AAY49892	Aay49892 RTM with
36	1325	98.5	265 2 AAY49890	Aay49890 Escherich
37	1325	98.5	265 4 AAE06924	Aae06924 E. coli T
38	1325	98.5	265 4 AAE06922	Aae06922 E. coli T
39	1325	98.5	265 5 AAM51111	Aam51111 Escherich
40	1325	98.5	283 4 AAB62272	Aab62272 Heavy cha
41	1325	98.5	285 5 AAM51112	Aam51112 Escherich
42	1325	98.5	286 1 AAP90058	Aap90058 beta-lact
43	1325	98.5	286 2 AAY08233	Aay08233 E. coli R
44	1325	98.5	286 2 AAW48614	Aaw48614 Escherich
45	1325	98.5	286 2 AAW80733	Aaw80733 Amino aci

ALIGNMENTS

RESULT 1	AAE05544	AAE05544 standard; protein; 263 AA.
ID	AAE05544	
XX	AAE05544	
AC	AAE05544	
XX	AAE05544	
DT	24-SEP-2001	(first entry)
XX		
DE	E. coli mature TEM-1 beta-lactamase.	
XX		
KM	Interaction-dependent enzyme association; IdRA system; biosensor;	
KM	circularly permuted interaction-activated protein; marker protein;	
KM	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;	
KW	therapeutic; drug screening; thioredoxin; ampicillin resistance.	
XX		
OS	Escherichia coli.	
XX		
Key	Location/Qualifiers	
FT	Cleavage-site	27..28 /note="Break-point between alpha and omega fragments"
FT	Region	36..40 /note="Inter-sub-domain loop"
FT	Cleavage-site	38..39 /note="Break-point between alpha and omega fragments"
FT	Active-site	45 /note="Break-point between alpha and omega fragments"
FT	Cleavage-site	74..75 /note="Break-point between alpha and omega fragments"
FT	Cleavage-site	149..150 /note="Break-point between alpha and omega fragments"
FT	Cleavage-site	172..173 /note="Break-point between alpha and omega fragments"
FT	Region	189..204 /note="Inter-sub-domain loop"
FT	Cleavage-site	190..191 /note="Break-point between alpha and omega fragments"
FT	Cleavage-site	202..203 /note="Break-point between alpha and omega fragments"
FT	Cleavage-site	228..229 /note="Break-point between alpha and omega fragments"
PD	WO200151629-A2.	
XX	19-JUL-2001.	
PF	16-JAN-2001; 2001WO-US001651.	
XX	13-JAN-2000; 2000US-0175968P.	
PR	15-MAR-2000; 2000US-00526106.	

```

2A (PANO-) PANORAMA RES INC.
XX
XX Balint RF, Her J;
XX
XX WPI: 2001-451857/48.
DR
DR N-PSDB; AAD10411.
XX
XX Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.
XX
XX Claim 38; Fig 2; 1044p; English.
XX
XX The invention relates to new interaction-dependent enzyme association
CC (IDEA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The IDA systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is Escherichia coli
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu
XX
XX Sequence 263 AA;
SQ
Query Match 98.9%; Score 1330; DB 4; Length 263;
Best Local Similarity 98.9%; Pred. No. 1.9e-123;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
1 HETLVKXKADADOLGARVGYIELNLNGEILIESPRSEERPEPMSTFKYLCSAVLSRID 60
1 HETLVKXKADADOLGARVGYIELNLNGSKILIESRPERFERPMSTFKYLCSAVLSRID 60
1 HETLVKXKADADOLGARVGYIELNLNGSKILIESRPERFERPMSTFKYLCSAVLSRID 60
61 AGOEOLGRRIRHYSQNDLVEYSFVTEKHLLTDGMTVRLCSAAITWSDNTPAANILLTTICGP 120
61 AGOEOLGRRIRHYSQNDLVEYSFVTEKHLLTDGMTVRLCSAAITWSDNTPAANILLTTICGP 120
61 AGOEOLGRRIRHYSQNDLVEYSFVTEKHLLTDGMTVRLCSAAITWSDNTPAANILLTTICGP 120
121 KELLTAFINMGHGVRLDWEPELNEALPNDSDRTTTPAAMTTLRKLLTGELTLASRQ 180
121 KELLTAFINMGHGVRLDWEPELNEALPNDSDRTTTPAAMTTLRKLLTGELTLASRQ 180
121 KELLTAFINMGHGVRLDWEPELNEALPNDSDRTTTPAAMTTLRKLLTGELTLASRQ 180
181 QLIDWMEADKVAQPLIRSAIPAGWFIADKSGGEGSGRRIIAALGPDGPKSRIVITYTG 240
181 QLIDWMEADKVAQPLIRSAIPAGWFIADKSGGEGSGRRIIAALGPDGPKSRIVITYTG 240
181 QLIDWMEADKVAQPLIRSAIPAGWFIADKSGGEGSGRRIIAALGPDGPKSRIVITYTG 240
241 SQATIDERNRQIAETIGASLILEM 263

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Db	241 SQATMDERNQRLAIEIGASLLIKHW	263
	RESULT 2	
AAAB36692	AAB36692 standard; protein; 263 AA.	
AC		
XX	AAB36692;	
XX		
DT	15-MAR-2001 (first entry)	
XX		
DE	Escherichia coli mature TEM-1 beta-lactamase protein sequence.	
XX		
KW	Interaction-activated protein; beta-lactamase; protein interaction.	
XX		
OS	Escherichia coli.	
PV	WC0200071702-A1.	
PD	30-NOV-2000.	
FX	16-MAR-2000; 2000WO-US007108.	
PF		
PR	25-MAY-1999; 99US-0135926P.	
PR	13-JAN-2000; 2000US-0175968P.	
PA	(PANO-) PANORAMA RES INC.	
PI	Balint RF, Her J;	
DR	WPI; 2001-032034/04.	
N-PSDB;	AAC90773.	
PT	Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable signal.	
PS	Disclosure; Fig 2; 94pp; English.	
CC	The present invention describes a fragment complementation system (I) which comprises a first oligopeptide (OP1) containing an N-terminal fragment with a C-terminal break point and a second oligopeptide (OP2) comprising a C-terminal with a N-terminal breakpoint, in which the C and N terminal fragments are both derived from a marker protein (MP) and reassemble to form a functionally reconstructed MP. Methods from the present invention are used for monitoring the occurrence of protein-protein interactions in a sample, identifying epitopes that bind to a protein between two different proteomes, identifying epitopes that bind to an immunoglobulin (Ig) variable region, for identifying interactions between an extracellular domain of a transmembrane protein and a polypeptide, for high-throughput identification of compounds that inhibit phosphorylation-regulated signal transducers, forming a enzyme complementation system for selecting simultaneous incorporation of multiple genetic elements into a host cell and for activating a beta-lactam derivative of an antitumor compound in a host who is in need of it. The present sequence represents the Escherichia coli mature TEM-1 beta-lactamase, which is used in the exemplification of the present invention	
SQ	Sequence 263 AA;	
Query Match	98.9%; Score 1330; DB 4; Length 263;	
Best Local Similarity	98.9%; Pred. No. 1.9e-129;	
Matches 260; Conservative	1; Mismatches 2; Indels 0; Gaps 0	
QY	1 HETTLVKVDADDOCGARYGYEELDNGSELTIESRSPSERPPMSTFKVLICGAVLSRID 60 	
Db	1 HETTLVKKADADDQCGARYGYEELDNGSKLIESRPERRFPMTTFKVILCGAVLSRID 60 	
QY	61 AGOEQLGRRIHYSQNDLVESFVTEKHLLTDGMTVEELCSAALTWSGNTAAILITIGGP 120 	
Db	61 AGOEOGLGRRIHYSQNDLVESFVTEKHLLTDGMTVEELCSAALTWSGNTAAILITIGGP 120 	

QY 121 KETLAFHNMGDHYTRLDRWEPELINEAI PNDERDTTPVAMATTIRKLLTGEILLTLASRQ 180
 Db 121 KETLAFHNMGDHYTRLDRWEPELINEAI PNDERDTTPVAMATTIRKLLTGEILLTLASRQ 180
 QY 181 QLIDMWEADKRVAGPLRSALPAGMFTADKSGAGERSGRTI AALGPDGKPSRIYVITYTG 240
 Db 181 QLIDMWEADKRVAGPLRSALPAGMFTADKSGAGERSGRTI AALGPDGKPSRIYVITYTG 240
 QY 241 SQATMDERNRQIAEIGASLIIKH 263
 Db 241 SQATMDERNRQIAEIGASLIIKH 263

RESULT 3

AAW16634
 ID AAW16634 standard; protein; 264 AA.
 AC AAW16634;
 XX
 DT 09-AUG-1997 (first entry)
 XX

DE Beta-lactamase (including signal peptide).
 XX
 KM Gene directed enzyme prodnug therapy; GDEPT;
 KM virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX

OS Escherichia coli.
 XX

PH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide
 XX

PN MO9719180-A2.
 XX

PD 29-MAY-1997.
 XX

PF 19-NOV-1996; 96MO-GB002845.
 XX

PR 20-NOV-1995; 95GB-00023703.
 XX

PA (GLAX) GLAXO GROUP LTD.
 XX

PI Dev I, Moore JT, Omstede C;
 XX

DR WPI; 1997-298117/27.
 XX

DR N-PSDB; AAT6736.
 XX

PT Molecular chimera for gene or virus directed enzyme prodnug therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX

PS Example; Page 28; 38pp; English.
 XX

CC Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated PCMY-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnug therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodnug into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill
 XX

SQ Sequence 264 AA;
 XX

Query Match 98.9%; Score 1330; DB 2; Length 264;
 Best Local Similarity 98.9%; Pred. No. 1.9e-129;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGETLSEFRSERRPMMSTFKVLLCGAVLSRID 60
 |||
 |||

Db 2 HPETLVKVKDAEDQLGARVGYIELDINSGETLSEFRSERRPMMSTFKVLLCGAVLSRID 61
 QY 61 AGGEQLGRRIRHYSONDLVYSPYTEKRLTDGMTVRELCSAATIMSDNTAANILLTTIGP 120
 Db 62 AGGEQLGRRIRHYSONDLVYSPYTEKRLTDGMTVRELCSAATIMSDNTAANILLTTIGP 121
 QY 121 KETLAFHNMGDHYTRLDRWEPELINEAI PNDERDTTPVAMATTIRKLLTGEILLTLASRQ 180
 Db 122 KETLAFHNMGDHYTRLDRWEPELINEAI PNDERDTTPVAMATTIRKLLTGEILLTLASRQ 181
 QY 181 QLIDMWEADKRVAGPLRSALPAGMFTADKSGAGERSGRTI AALGPDGKPSRIYVITYTG 240
 Db 182 QLIDMWEADKRVAGPLRSALPAGMFTADKSGAGERSGRTI AALGPDGKPSRIYVITYTG 241
 QY 241 SQATMDERNRQIAEIGASLIIKH 263
 Db 242 SQATMDERNRQIAEIGASLIIKH 264

RESULT 4

AAW18680
 ID AAW18680 standard; protein; 264 AA.
 XX

AC AAW18680;
 XX

DT 13-AUG-1997 (first entry)
 XX

DE Intracellularly-expressed beta-lactamase.
 XX

KM Prodnug therapy; gene directed enzyme prodnug therapy; GDEPT;
 KM virus directed enzyme prodnug therapy; VDEPT; lung cancer;
 KM beta-lactamase; PCMY-delBL.
 XX

OS Escherichia coli.
 XX

PN MO9719183-A2.
 XX

PD 29-MAY-1997.
 XX

PF 19-NOV-1996; 96MO-GB002846.
 XX

PR 20-NOV-1995; 95GB-00023703.
 XX

PA (GLAX) GLAXO GROUP LTD.
 XX

PI Dev I, Moore JT, Sethna PB;
 XX

DR WPI; 1997-298118/27.
 XX

DR N-PSDB; AAT70311.
 XX

PT DNA construct for gene-directed enzyme prodnug therapy of lung cancer -
 PT comprises lung- or neuroendocrine-specific promoter controlling
 PT expression of prodnug-converting enzyme.
 XX

PS Example 811; Page 32-34; 53pp; English.
 XX

CC The intracellular form (AAW18680) of TEM beta-lactamase is expressed by
 CC PCMY-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
 CC sequence, minus the signal sequence, is placed under control of the
 CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
 CC lactamase constructs, placed under control of promoter/enhancer elements
 CC of lung-associated protein or neuroendocrine marker protein genes, can be
 CC used in novel chimeraic molecules for use in prodnug therapy of lung
 CC cancer
 XX

SQ Sequence 264 AA;
 XX

Query Match 98.9%; Score 1330; DB 2; Length 264;
 Best Local Similarity 98.9%; Pred. No. 1.9e-129;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGETLSEFRSERRPMMSTFKVLLCGAVLSRID 60
 |||
 |||

Db 2 HPEITVVKVKAEDOLGARVGYIELDLSNGKILSFREPERPMMSTFKVLLCGAVLSRID 61
 QY 61 AGGEQLGRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATWSDNTAANLLITTTGGP 120
 Db 62 AGGEQLGRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATWSDNTAANLLITTTGGP 121
 QY 121 KELTSAPLHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVMAATLRLKLTGELLTLASRQ 180
 Db 122 KELTSAPLHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVMAATLRLKLTGELLTLASRQ 181
 QY 181 QLIDMEADKVAAGPLRSALPAGWFIADKSGAGRSRGIIAALGPDGKPSRIIVITYTG 240
 Db 182 QLIDMEADKVAAGPLRSALPAGWFIADKSGAGRSRGIIAALGPDGKPSRIIVITYTG 241
 QY 241 SQATMDERNROIATIGASLIKHW 263
 Db 242 SQATMDERNROIATIGASLIKHW 264

RESULT 5
 AAR31575
 ID AAR31575 standard; protein; 286 AA.
 XX
 AC AAR31575;
 DT 10-MAR-2003 (revised)
 DT 04-JUN-1993 (first entry)
 XX
 DE Ampicillin resistance protein.
 XX
 KM CYPLA1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;
 KM xenobiotics; circular; chimeric cytochrome P450IA1.
 XX
 OS Homo sapiens.
 XX US5180666-A.
 XX 19-JAN-1993.
 PD 19-JAN-1993.
 PF 27-JUN-1991; 91US-00721775.
 XX 27-JUN-1991;
 PR 27-JUN-1991; 91US-00721775.
 XX
 PA (UYMA-) UNITV WAYNE STATE.
 XX
 PI States JC, Hines RN, Novak RF;
 XX
 DR MPI; 1993-052845/06.
 DR N-PSDB; AAQ36498.
 XX
 PT In vitro method for testing mutagenicity of a chemical - by metabolising
 PT chemical cell line consisting of transformed fibroblasts having
 PT detectable cytochrome P450 mixed function oxidase activity and detecting
 PT gene damage.
 XX
 PS Disclosure; Col 21-24; 24pp; English.
 XX
 XX The expression constructs pRNH127 and pRNH155 contain identical sequences
 CC but were constructed using different strategies (see AAQ36498). The
 CC constructs comprise exons 2-7 of human CYPLA1 gene under the control of
 CC the inducible mouse metallothionein (MMT-1) promoter. The constructs also
 CC contain an open reading frame in the opposite orientation to the
 CC cytochrome P450 exons. This ORF encodes ampicillin resistance. The
 CC constructs are suitable for transformation of human fibroblasts derived
 CC from the xeroderma pigmentosum group A. Cultures of the transformed
 CC fibroblasts can be used to test substances for mutagenicity. The presence
 CC of the inducible cytochrome P450 gene allows metabolism of the substance
 CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
 CC field.)
 CC
 SQ Sequence 286 AA;
 Query Match 98.9%; Score 1330; DB 2; Length 286;

Best Local Similarity 98.9%; Pred. No. 2.2e-129;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVVKVKAEDOLGARVGYIELDLSNGKILSFREPERPMMSTFKVLLCGAVLSRID 60
 Db 24 HPEITVVKVKAEDOLGARVGYIELDLSNGKILSFREPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGEQLGRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATWSDNTAANLLITTTGGP 120
 Db 84 AGGEQLGRRIHYSQNDLVEYSPTYEKHLTDGMTVRELCSAATWSDNTAANLLITTTGGP 143
 QY 121 KELTSAPLHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVMAATLRLKLTGELLTLASRQ 180
 Db 144 KELTSAPLHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVMAATLRLKLTGELLTLASRQ 203
 QY 181 QLIDMEADKVAAGPLRSALPAGWFIADKSGAGRSRGIIAALGPDGKPSRIIVITYTG 240
 Db 204 QLIDMEADKVAAGPLRSALPAGWFIADKSGAGRSRGIIAALGPDGKPSRIIVITYTG 263
 QY 241 SQATMDERNROIATIGASLIKHW 263
 Db 264 SQATMDERNROIATIGASLIKHW 286

RESULT 6
 AAR97619
 ID AAR97619 standard; protein; 286 AA.
 XX
 AC AAR97619;
 DT 20-AUG-1996 (first entry)
 DT
 XX
 DE Secretory beta-lactamase.
 XX
 KM Gene therapy; gene directed enzyme prodng therapy; GDEPT;
 KM virus directed enzyme prodng therapy; VDEPT; prodng activation;
 KM cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
 KM beta-lactamase; cephalosporin.
 XX
 OS Synthetic.
 XX WO9616179-A1.
 EN 30-MAY-1996.
 PD 30-MAY-1996.
 PF 20-NOV-1995; 95MO-GB002716.
 XX 20-NOV-1995;
 PR 18-NOV-1994; 94GB-00023367.
 XX
 PA (WELL) WELLCOME FOUND LTD.
 XX
 PI Dev IX, Moore JT, Chmstede C;
 XX
 DR MPI; 1996-268615/27.
 DR N-PSDB; AAT29220.
 XX
 PT Molecular chimera for use in enzyme gene therapy - is activated in a
 PT target cell to express a secretable enzyme which cleaves a prodng
 PT outside the cell into a cytotoxic or cytostatic agent.
 XX
 PS Example 3; Page 57-58; 73pp; English.
 XX
 XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct
 CC PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under
 CC the control of the intermediate/early cytomegalovirus promoter. Beta-
 CC lactamase delivery to mammalian cells confers sensitivity to
 CC cephalosporin prodngs. Liposomal DNA/5-fluorouracil prodng combinations
 CC resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
 CC of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
 CC was increased upon i.t. injection of the secretory beta-lactamase DNA
 CC construct.
 CC
 SQ Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;
 Best Local Similarity 98.9%; Pred. No. 2.2e-129;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGRVGIIELDLSGELISFRSEERPPMSTFKVILCGAVLSRID 60
 DB 24 HPEITLVKKAEDQAGRVGIIELDLSGELISFRSEERPPMSTFKVILCGAVLSRID 83
 QY 61 AGGEOGRRIHYSQNDLVEYSPVTEKHLTDGMTVREICSAATMSDNTAANLLTTTGGP 120
 DB 84 AGGEOGRRIHYSQNDLVEYSPVTEKHLTDGMTVREICSAATMSDNTAANLLTTTGGP 143
 QY 121 KELTAFIHHNGDHTVTRLDREPELNEAIPNDEEDTTTPVAMATTIRKLTGELLTLASRQ 180
 DB 144 KELTAFIHHNGDHTVTRLDREPELNEAIPNDEEDTTTPVAMATTIRKLTGELLTLASRQ 203
 QY 181 QLIDWMEADKVPGLRLSALPAGWFIADKSGAGERSGRIIAGLPGDKPSRIIVITYTG 240
 DB 204 QLIDWMEADKVPGLRLSALPAGWFIADKSGAGERSGRIIAGLPGDKPSRIIVITYTG 263
 QY 241 SQATMDERNRQIAEIGASLIIKHW 263
 DB 264 SQATMDERNRQIAEIGASLIIKHW 286

RESULT 7
 AAR96423
 ID AAR96423 standard; protein; 286 AA.
 AC AAR96423;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-NOV-1996 (first entry)
 XX
 DE Cytochrome P450 (CYP1A1 construct).
 XX
 KW cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
 KM metabolism.
 XX
 OS Homo sapiens.
 XX
 PN US5525482-A.
 PD 11-JUN-1996.
 XX
 PF 15-NOV-1994; 94US-00339658.
 XX
 PR 27-JUN-1991; 91US-00721775.
 PR 09-DEC-1992; 92US-0090295.
 XX
 PA (UYMA-) UNIV MAYNE STATE.
 XX
 PI Hines RN, Novak RF, States JC;
 XX
 DR WPI; 1996-286397/29.
 DR N-PSDB; AAT30354.
 XX
 PT Testing chemicals for cytotoxicity to human by detecting gene damage -
 PT using recombinant fibroblasts transformed with cytochrome P450 gene under
 PT control of inducible promoter.
 XX
 PS Disclosure; Col 17-24; 26pp; English.
 XX
 CC The present sequence is encoded by a chimeric mouse metallothionein-
 CC cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNH127 and
 CC pRNH15, were isolated by different methods and which both had the same
 CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
 CC of humans to a chemical. The method comprises exposing human fibroblast
 CC cells normally not including any cytochrome P450 activity to potentially
 CC toxic chemicals. The cells having been transformed to express cytochrome
 CC P450, under the control of a controllable promoter through the CYP1A1
 CC gene, upon exposure to the chemical in vitro. The chemical is metabolised

CC intracellularly into a cytochrome metabolite by oxidation within the
 CC fibroblasts through the intracellular cytochrome P450 mixed function
 CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
 CC detected as an indication of cytotoxicity of the chemical. (updated on 25
 CC -MAR-2003 to correct PF field.)
 XX
 SQ Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;
 Best Local Similarity 98.9%; Pred. No. 2.2e-129;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGRVGIIELDLSGELISFRSEERPPMSTFKVILCGAVLSRID 60
 DB 24 HPEITLVKKAEDQAGRVGIIELDLSGELISFRSEERPPMSTFKVILCGAVLSRID 83
 QY 61 AGGEOGRRIHYSQNDLVEYSPVTEKHLTDGMTVREICSAATMSDNTAANLLTTTGGP 120
 DB 84 AGGEOGRRIHYSQNDLVEYSPVTEKHLTDGMTVREICSAATMSDNTAANLLTTTGGP 143
 QY 121 KELTAFIHHNGDHTVTRLDREPELNEAIPNDEEDTTTPVAMATTIRKLTGELLTLASRQ 180
 DB 144 KELTAFIHHNGDHTVTRLDREPELNEAIPNDEEDTTTPVAMATTIRKLTGELLTLASRQ 203
 QY 181 QLIDWMEADKVPGLRLSALPAGWFIADKSGAGERSGRIIAGLPGDKPSRIIVITYTG 240
 DB 204 QLIDWMEADKVPGLRLSALPAGWFIADKSGAGERSGRIIAGLPGDKPSRIIVITYTG 263
 QY 241 SQATMDERNRQIAEIGASLIIKHW 263
 DB 264 SQATMDERNRQIAEIGASLIIKHW 286

RESULT 8
 AAM16635
 ID AAM16635 standard; protein; 286 AA.
 AC AAM16635;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (no signal peptide).
 XX
 KW Gene directed enzyme prodnug therapy; GDEPT;
 KW virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 PN WO9719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96MO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmsted C;
 XX
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66737.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodnug therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 26; 38pp; English.
 XX
 CC Escherichia coli beta-lactamase (AAM16635), lacking the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Intracellular expression of the beta-lactamase in
 CC a targeted cell allows conversion of a prodrug into an agent toxic to
 CC the cell for treatment of cancer. Viral (e.g. HIV) infection or
 CC inflammation

XX Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;
 Best Local Similarity 98.9%; Pred. No. 2.2e-129;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGRVGIEIDLSNGELLEFSRSEPRPMSTFKVILCGAVLSRID 60
 DB 24 HPEITLVKVAEDQAGRVGIEIDLSNGELLEFSRSEPRPMSTFKVILCGAVLSRID 83
 QY 61 AGGQQLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAAILTTTGGP 120
 DB 84 AGGQQLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAAILTTTGGP 143
 QY 121 KETLAFILHNMGDHVTRLDRWEPELNEAIPNDERDTTPVMAATTLRKILTGELLTLASRQ 180
 DB 144 KETLAFILHNMGDHVTRLDRWEPELNEAIPNDERDTTPVMAATTLRKILTGELLTLASRQ 203
 QY 181 QLTIMMEADKVAGPLLSALPAGWFIDKSGAGRGSGRIITAIAGPDGKPSRIIVITYTG 240
 DB 204 QLTIMMEADKVAGPLLSALPAGWFIDKSGAGRGSGRIITAIAGPDGKPSRIIVITYTG 263
 QY 241 SQATMDERNRQIAETGASLIKHW 263
 DB 264 SQATMDERNRQIAETGASLIKHW 286

RESULT 9

AAW18679
 ID AAW18679 standard; protein; 286 AA.

AC AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

KM Producing therapy; gene directed enzyme producing therapy; GDEPT;

KW virus directed enzyme producing therapy; VDEPT; lung cancer;

KX beta-lactamase; PCMV-BL.

OS Escherichia coli.

XX Key location/Qualifiers

XX Peptide 1..23

XX Protein 24..286

XX WO9719183-A2.

XX PD 29-MAY-1997.

XX PF 19-NOV-1996; 96WO-GB002846.

XX PR 20-NOV-1995; 95GB-00023703.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Dev I, Moore JT, Sethna PB;

XX DR N-PSDB; AAT70309.

XX WPI: 1997-298118/27.

PT DNA construct for gene-directed enzyme producing therapy of lung cancer -
 PT comprises lung- or neuroendocrine-specific promoter controlling
 PT expression of prodrug-converting enzyme.

XX Example 811; Page 26-27; 53pp; English.

PS The secreted form (AAW18679) of TEM beta-lactamase is expressed by PCMV-
 CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
 CC placed under control of the intermediate/early promoter of
 CC cytomegalovirus. Secretory beta-lactamase constructs, placed under
 CC control of promoter/enhancer elements of lung-associated protein or
 CC neuroendocrine marker protein genes, can be used in novel chemotherapeutic
 CC molecules for use in prodrug therapy of lung cancer

XX Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;
 Best Local Similarity 98.9%; Pred. No. 2.2e-129;
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGRVGIEIDLSNGELLEFSRSEPRPMSTFKVILCGAVLSRID 60
 DB 24 HPEITLVKVAEDQAGRVGIEIDLSNGELLEFSRSEPRPMSTFKVILCGAVLSRID 83
 QY 61 AGGQQLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAAILTTTGGP 120
 DB 84 AGGQQLGRRIHYSQNDIVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAAILTTTGGP 143
 QY 121 KETLAFILHNMGDHVTRLDRWEPELNEAIPNDERDTTPVMAATTLRKILTGELLTLASRQ 180
 DB 144 KETLAFILHNMGDHVTRLDRWEPELNEAIPNDERDTTPVMAATTLRKILTGELLTLASRQ 203
 QY 181 QLTIMMEADKVAGPLLSALPAGWFIDKSGAGRGSGRIITAIAGPDGKPSRIIVITYTG 240
 DB 204 QLTIMMEADKVAGPLLSALPAGWFIDKSGAGRGSGRIITAIAGPDGKPSRIIVITYTG 263
 QY 241 SQATMDERNRQIAETGASLIKHW 263
 DB 264 SQATMDERNRQIAETGASLIKHW 286

RESULT 10

AAV08529
 ID AAV08529 standard; protein; 286 AA.

AC AAV08529;

DT 03-AUG-1999 (first entry)

DE Vector pASK75 beta-la protein.

XX Firefly, luciferase; tetracycline; transcriptional control; TetR; TetA;

KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;

KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;

XX Synthetic.

XX WO9925866-A1.

XX PD 27-MAY-1999.

XX PF 11-NOV-1998; 98WO-FI000873.

XX ER 14-NOV-1997; 97FI-00004235.

XX PA (KORP/) KORBELA M.

XX PA (KARP/) KARP M.

XX PA (KURIT) KURIT J.

XX PI Korpela M, Karp M, Kurittu J;

XX DR WPI: 1999-338015/28.

XX DR N-PSDB; AAV72418.

XX Assaying for tetracycline using recombinant prokaryotic cells.

XX Disclosure; Page 47-48; 67pp; English.
PS
XX
CC This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline form other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxDABE
CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetP)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (TetR)
CC and a tetracycline promoter (TetP) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,
CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected
XX
SQ Sequence 286 AA;
Query Match 98.9%; Score 1330; DB 2; Length 286;
Best Local Similarity 98.9%; Pred. No. 2.2e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQDQAGRVYIELDNSGELISFRSEERFPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQDQAGRVYIELDNSGELISFRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEOUGRRIRHYSQNDLVESPYTEKHLTDGKTVRELCSAITMSDNTANLLTTTGGP 120
Db 84 AGGEOUGRRIRHYSQNDLVESPYTEKHLTDGKTVRELCSAITMSDNTANLLTTTGGP 143
QY 121 KETLTAFLHNMGDVTRLDREPELNEAIPNDERDITTPVAMATTIRKLTLGELLTLASRQ 180
Db 144 KETLTAFLHNMGDVTRLDREPELNEAIPNDERDITTPVAMATTIRKLTLGELLTLASRQ 203
QY 181 QLIDWMEADKVGAPLLRSALPAGWFIADKSGAGERSGGIIAALGPDGKPSRIIVYITTG 240
Db 204 QLIDWMEADKVGAPLLRSALPAGWFIADKSGAGERSGGIIAALGPDGKPSRIIVYITTG 263
QY 241 SQATMDERNRQIAETIGASLTKHW 263
Db 264 SQATMDERNRQIAETIGASLTKHW 286
RESULT 11
AAB10442
ID AAB10442 standard; protein; 286 AA.
XX
AC AAB10442;
XX
DT 01-DEC-2000 (first entry)
XX
DE Expression vector pSEX1562 bla protein.
XX
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
OS Synthetic.
XX
PN DE19900635-A1.
XX
PD 13-JUL-2000.
XX
PF 11-JAN-1999; 99DE-01000635.
XX
PR 11-JAN-1999; 99DE-01000635.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX
PI Breitling F, Poustcka A, Moldenhauer G;
XX
DR WPI; 2000-499832/45.
XX
DR N-PSDB; AAA71430.
XX
PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
PS Claim 16; Fig 3; 22pp; German.
XX
CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX1562 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
SQ Sequence 286 AA;
Query Match 98.9%; Score 1330; DB 3; Length 286;
Best Local Similarity 98.9%; Pred. No. 2.2e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQDQAGRVYIELDNSGELISFRSEERFPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQDQAGRVYIELDNSGELISFRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEOUGRRIRHYSQNDLVESPYTEKHLTDGKTVRELCSAITMSDNTANLLTTTGGP 120
Db 84 AGGEOUGRRIRHYSQNDLVESPYTEKHLTDGKTVRELCSAITMSDNTANLLTTTGGP 143
QY 121 KETLTAFLHNMGDVTRLDREPELNEAIPNDERDITTPVAMATTIRKLTLGELLTLASRQ 180
Db 144 KETLTAFLHNMGDVTRLDREPELNEAIPNDERDITTPVAMATTIRKLTLGELLTLASRQ 203
QY 181 QLIDWMEADKVGAPLLRSALPAGWFIADKSGAGERSGGIIAALGPDGKPSRIIVYITTG 240
Db 204 QLIDWMEADKVGAPLLRSALPAGWFIADKSGAGERSGGIIAALGPDGKPSRIIVYITTG 263
QY 241 SQATMDERNRQIAETIGASLTKHW 263
Db 264 SQATMDERNRQIAETIGASLTKHW 286
RESULT 12
AAB10438
ID AAB10438 standard; protein; 286 AA.
XX
AC AAB10438;
XX
DT 01-DEC-2000 (first entry)
XX
DE Expression vector pSEX1114 bla protein.
XX
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
OS Synthetic.
XX

PN	DE19000635-A1.
XX	
PD	13-JUL-2000.
XX	
PF	11-JAN-1999; 99DE-01000635.
XX	
PR	11-JAN-1999; 99DE-01000635.
XX	
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX	
PI	Breitling F, Poustka A, Moldenhauer G;
XX	
DR	WPI; 2000-499632/45.
DR	N-PSTDB; AAA71428.
XX	
PT	Selecting monoclonal antibodies, by expressing them on the surface of
PT	hybridomas attached to antibody-binding protein, then reaction with
PT	antibody library.
XX	
PS	Claim 16; Fig 1; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) class I k (k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the Neo-R
CC protein contained in the expression vector pEXk14 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
CC Sequence 286 AA;

Query Match	98.9%	Score 1330;	DB 3;	Length 286;
Best Local Similarity	98.9%	Pred. No. 2.2e-129;		
Matches 260; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	HEETLVKVDADPOLGARVGYIELDINSGBIESFSESEFPMMSTFKVLLCGAVLSRID	60
Db	24	HEETLVKVDADPOLGARVGYIELDINSGBIESFSESEFPMMSTFKVLLCGAVLSRID	83
QY	61	AGQEOIGRIIHSQNDLVESPVTEKHLTDGMTVRELCSAITSMDTANLLITTTGGP	120
Db	84	AGQEOIGRIIHSQNDLVESPVTEKHLTDGMTVRELCSAITSMDTANLLITTTGGP	143
QY	121	KELTAFILHMGVHVRLDKMEPELNAIPNDERDITTPVAMATTLTKRLTIGELLTTSARQ	180
Db	144	KELTAFILHMGVHVRLDKMEPELNAIPNDERDITTPVAMATTLTKRLTIGELLTTSARQ	203
QY	181	QLIDWNEADKVGAPLRSALPAGMFIADKSGAGERSGRIIALGPDGKPSRIWVITYTTG	240
Db	204	QLIDWNEADKVGAPLRSALPAGMFIADKSGAGERSGRIIALGPDGKPSRIWVITYTTG	263
QY	241	SOATMDERRQTAIEIGASLIKHW	263
Db	264	SOATMDERRQTAIEIGASLIKHW	286

```
RESULT 13
AAB10440
ID AAB10440 standard; protein; 286 AA
XX
XX AC AAB10440;
XX
```

DT	01-DEC-2000	(first entry)
XX		
DE	Expression vector pSEX1IG2 bla protein.	
XX		
XX	Expression vector; antibody binding protein; monoclonal antibody; Neo-R;	
KW	B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.	
XX		
XX		
OS	Synthetic.	
XX		
PN	DE19900635-A1.	
XX		
PD	13-JUL-2000.	
XX		
XX		
PF	11-JAN-1999;	99DE-01000635.
XX		
PR	11-JAN-1999;	99DE-01000635.
XX		
XX		
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
FI	Breitling F, Poustka A, Moldenhauer G;	

PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.
PS Claim 16; Fig 2; 22pp; German.

This invention describes a novel method for the selection of monoclonal antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(x) molecule; or an antibody-binding site of proteins A, G, I or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and costs involved in Mab selection. This sequence represents the bla protein contained in the expression vector pEX1162 which contains the bla protein, Neo-R and protein G described in the method of the invention.

Query Match	98.9%;	Score 1330;	DB 3;	Length 286;
Best Local Similarity	98.9%;	Pred. No. 2,2e-129;		
Matches 260; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0

```

QY      HETTLVKYKADADDOCGARVGYIELDNLSGEILSFSSSEEPFMSTFEKVLCCAVLSRID    60
Db      HETTLVKRKADADDOCGARVGYIELDNLSKILSFSEEPFERFPMSTFEKVLCCAVLSRID    83
QY      61 AGOEOLGRRIRYKSONDLVYSPTYEKHLTDGMTVRLCSAALMSONTANLLITTTGGP    12
Db      84 AGOEOLGRRIRYKSONDLVYSPTYEKHLTDGMTVRLCSAALMSONTANLLITTTGGP    14
QY      121 KELLTAFLNHMGDHYVRLDRWEPELNELAIENDEEDITTPYAMATTTKRLTGLBLLTASRQ    18
Db      144 KELLTAFLNHMGDHYVRLDRWEPELNELAIENDEEDITTPYAMATTTKRLTGLBLLTASRQ    20
QY      181 QLIIDMEALYKVGPLLRSLPAQWFLADKSGAERGSRGIIAALGPGKRSRIYVITYTG    24
Db      204 QLIIDMEALYKVGPLLRSLPAQWFLADKSGAERGSRGIIAALGPGKRSRIYVITYTG    26
QY      241 SQATMDERNRQIAETGASLLIKHW    263

```

Db 264 SQATMDERNQIAEIGASLIKHW 286

RESULT 14
AAB50898
ID AAB50898 standard; protein; 286 AA.
XX
AC AAB50898;
XX
DT 20-MAR-2001 (first entry)
XX
DE Protein encoded by bla resistance marker of integration vector pLO12306.
XX
KM bla resistance marker; recombinant host cell; saccharification;
KM fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KM glucanase; integration vector; pLO12306.
XX
OS Unidentified.
XX
PN WO200071729-A2.
XX
PD 30-NOV-2000.
XX
PF 26-MAY-2000; 2000WO-US014773.
XX
PR 26-MAY-1999; 99US-0136376P.
XX
PA (UYFL) UNIV FLORIDA RES FOUND.
XX
PI Ingram LO, Zhou S;
XX
DR WPI; 2001-032043/04.
DR N-PSDB; AAC91455.
XX
PT Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.
XX
PS Disclosure; Page 82-83; 87pp; English.
XX
CC The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC *chrysanthemi*, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence
XX
SQ Sequence 286 AA;
Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 2.2e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVVKYKADBDQUGARVGYIELDNGSGLIESFRSEFPFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVVKYKADBDQUGARVGYIELDNGSGLIESFRSEFPFPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSNDIVESPYTEKHLDGQTVRELGSAAITMGDNTNANILTTTIGCP 120
DB 84 AGOEOLGRRIRHSNDIVESPYTEKHLDGQTVRELGSAAITMGDNTNANILTTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDNRWEPLEINAI PNDERDTTTPVAMATTLRLTGELITLARSQ 180

Db 144 KELTAFILNMGDHYTRLDNRWEPLEINAI PNDERDTTTPVAMATTLRLTGELITLARSQ 203

QY 181 QLIDWMEADKVAGPILRSALPAGMFIADKSGAGERSGRIIAALGPDGKSRIVVYTTG 240
DB 204 QLIDWMEADKVAGPILRSALPAGMFIADKSGAGERSGRIIAALGPDGKSRIVVYTTG 263

QY 241 SQATMDERNQIAEIGASLIKHW 263
DB 264 SQATMDERNQIAEIGASLIKHW 286

RESULT 15
AAB31173
ID AAB31173 standard; protein; 286 AA.
XX
AC AAB31173;
XX
DT 02-APR-2001 (first entry)
XX
DE Amino acid sequence of a beta lactamate protein.
XX
KM Growth rate; death rate; reporter gene; luminescent protein;
KM fluorescent product; luciferase; green fluorescent protein; GFP.
XX
OS Unidentified.
XX
PN WO200075367-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-FI000507.
XX
PR 07-JUN-1999; 99FI-00001296.
XX
PA (LILI/) LILIUS E.
PA (VIRT/) VIRT M.
XX
PI Lilius E, Virta M;
XX
DR WPI; 2001-061737/07.
DR N-PSDB; AAC86954.
XX
PT Assessing growth and death rates of a micro-organism in a desired
PT environment, by introducing 2 reporter genes encoding luminescent and
PT fluorescent products and detecting luminescent fluorescence.
XX
PS Disclosure; Page 28-29; 32pp; English.
XX
CC The specification describes a method for assessing the growth rate and
CC death rate of a micro-organism within a predetermined time period in a
CC desired environment. The method comprises introducing at least two
CC reporter genes encoding luminescent and/or fluorescent products into the
CC micro-organisms, incubating the micro-organism within the desired
CC environment, and detecting luminescence and/or fluorescence after a
CC predetermined time period. Use of two different markers within a micro-
CC organism enables the differentiation between growth and death rates. The
CC method is used to assess the growth rate and death rate of a micro-
CC organism within a predetermined time period in a desired environment. The
CC present sequence represents a beta-lactamate protein, and is encoded by a
CC plasmid which encodes luminescent and fluorescent proteins, and is used
CC in the method of the invention
XX
SQ Sequence 286 AA;
Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 2.2e-129;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITVVKYKADBDQUGARVGYIELDNGSGLIESFRSEFPFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVVKYKADBDQUGARVGYIELDNGSGLIESFRSEFPFPMSTFKVLLCGAVLSRID 83

QY	61	AGQOLGRRIHYSQNDIVESPTTEKHLTDGMTVRELCSAITMSDNTAANLLTTIGP	120
Db	84	AGQOLGRRIHYSQNDIVESPTTEKHLTDGMTVRELCSAITMSDNTAANLLTTIGP	143
QY	121	KELTAFLHNNMGDHYTRLDRWEPELNEAI PNDERDPTTPVAMATTIRKILGELLTLASRQ	180
Db	144	KELTAFLHNNMGDHYTRLDRWEPELNEAI PNDERDPTTPVAMATTIRKILGELLTLASRQ	203
QY	181	QIIPWMEADKVAAGPLLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG	240
Db	204	QIIPWMEADKVAAGPLLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVITYTG	263
QY	241	SOATMDERNROIATIGASLIKHW	263
Db	264	SOATMDERNROIATIGASLIKHW	286

Search completed: June 18, 2004, 19:08:00
 Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:08:33 ; Search time 20 Seconds

(without alignments)
594.865 Million cell updates/sec

Title: EPPR526106.PEP

Sequence: 1 hpetlykvkaedqlgary.....tmdermqiaegslkhw 263

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 294345 seqs, 45236911 residues

Total number of hits satisfying chosen parameters: 294345

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_AA_New:*
1: /cgn2_6/pcodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/pcodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/pcodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/pcodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/pcodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/pcodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/pcodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330	98.9	286	5	US-09-490-324-265 Sequence 265, App
2	1330	98.9	286	5	US-09-490-324-362 Sequence 362, App
3	1330	98.9	286	6	US-10-416-708A-73 Sequence 73, Appl
4	1330	98.9	286	6	US-10-045-674A-523 Sequence 523, Appl
5	1330	98.9	299	5	US-09-490-324-285 Sequence 285, App
6	1330	98.9	299	5	US-09-490-324-298 Sequence 298, App
7	1329	98.8	286	6	US-09-490-324-300 Sequence 300, Appl
8	1329	98.8	1293	6	US-10-842-534-9 Sequence 9, Appl
9	1329	98.8	265	6	US-10-668-035-57 Sequence 57, Appl
10	1329	98.8	498	6	US-10-622-088-114 Sequence 114, App
11	1302	96.8	306	6	US-10-491-653-146 Sequence 146, App
12	343.5	25.5	290	6	US-10-724-972A-6154 Sequence 6154, App
13	175	11.0	290	6	US-10-414-532-65 Sequence 65, Appl
14	137	10.2	334	6	US-10-453-372-332 Sequence 332, App
15	137	10.2	841	6	US-10-453-372-334 Sequence 334, App
16	109	8.1	21	6	US-10-414-533-3 Sequence 3, Appl
17	107.5	8.0	524	6	US-10-414-533-28 Sequence 28, Appl
18	102	7.6	432	1	PCT-US04-12717-118 Sequence 118, App
19	102	7.6	432	7	US-10-831-070-118 Sequence 118, App
20	102	7.6	432	7	US-60-546-745-58 Sequence 58, Appl
21	98	7.3	550	7	US-60-556-841-6264 Sequence 6264, App
22	98	7.3	552	7	US-60-556-841-3455 Sequence 3455, App
23	95.5	7.1	561	6	US-10-796-280-761 Sequence 761, Appl
24	94.5	7.0	410	6	US-10-474-792-99 Sequence 90, Appl
25	90	6.7	507	7	US-60-556-841-406 Sequence 406, Appl
26	90	6.7	1217	1	PCT-US04-02188-101 Sequence 101, App

27	90	6.7	1217	6	US-10-764-425-101	Sequence 101, App
28	89.5	6.7	363	7	US-60-556-841-4337	Sequence 4337, App
29	88.5	6.6	494	6	US-10-494-495-13	Sequence 13, Appl
30	87	6.5	451	6	US-10-474-792-390	Sequence 390, App
31	86.5	6.4	438	5	US-09-248-796A-19853	Sequence 19853, App
32	85.5	6.4	358	7	US-60-556-841-11741	Sequence 11741, A
33	85.5	6.4	551	6	US-10-767-701-45690	Sequence 45690, A
34	85	6.3	411	6	US-10-091-007A-190	Sequence 190, App
35	84.5	6.3	363	7	US-60-556-841-2715	Sequence 2715, App
36	84.5	6.3	363	7	US-60-556-841-2715	Sequence 2715, App
37	84.5	6.3	363	7	US-60-556-841-2715	Sequence 2715, App
38	83.5	6.2	331	6	US-10-494-672-294	Sequence 294, App
39	83.5	6.2	439	5	US-09-248-796A-19522	Sequence 19522, A
40	83	6.2	218	6	US-10-767-701-39284	Sequence 39284, A
41	82.5	6.1	657	7	US-60-556-841-6693	Sequence 6693, App
42	82	6.1	320	6	US-10-472-317-37	Sequence 37, Appl
43	82	6.1	421	7	US-60-556-841-12214	Sequence 12214, A
44	82	6.1	606	7	US-60-556-841-3226	Sequence 3226, App
45	81.5	6.1	314	1	PCT-US03-02038-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-490-324-265

Sequence 265, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Laming

Moreney, Simon

Plueckehun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-490-324-265

Sequence 265, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Laming

Moreney, Simon

Plueckehun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

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ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-490-324-265

Sequence 265, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Laming

Moreney, Simon

Plueckehun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-490-324-265

Sequence 265, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Laming

Moreney, Simon

Plueckehun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Best Local Similarity 98.9%; Pred. No. 1.7e-119; Indels 0; Gaps 0;
Matches 260; Conservative 1; Mismatches 2;

QY 1 HPELVKVDADQOLGARVGYIELDNSGELLESFRSEERFPMMSTFKVLLCGAVLSRID 60
Db HPELVKVDADQOLGARVGYIELDNSGELLESFRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 120
Db AGOEOLGRRIHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 143
QY 121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGEILLTASRQ 180
Db KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGEILLTASRQ 203
QY 144 QLIDWMEADKVAQPLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTG 240
Db QLIDWMEADKVAQPLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNQIAEIGASLIKHW 263
Db SQATMDERNQIAEIGASLIKHW 286

RESULT 2

US-09-490-324-362
Sequence 362, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

pack, Peter

ilag, vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9090

TELEFAX: (212)596-9000

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-324-362
Query Match 98.9%; Score 1330; DB 5; Length 286;

Best Local Similarity 98.9%; Pred. No. 1.7e-119; Indels 0; Gaps 0;
Matches 260; Conservative 1; Mismatches 2;

QY 1 HPELVKVDADQOLGARVGYIELDNSGELLESFRSEERFPMMSTFKVLLCGAVLSRID 60
Db HPELVKVDADQOLGARVGYIELDNSGELLESFRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 120
Db AGOEOLGRRIHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 143
QY 121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGEILLTASRQ 180
Db KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGEILLTASRQ 203
QY 144 QLIDWMEADKVAQPLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTG 240
Db QLIDWMEADKVAQPLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNQIAEIGASLIKHW 263
Db SQATMDERNQIAEIGASLIKHW 286

RESULT 3

US-10-416-708A-73
Sequence 73, Application US/10416708A

GENERAL INFORMATION:

APPLICANT: Wise, John G.

FROM: Knappik, Achim

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING

FILE REFERENCE: 37779-0004

CURRENT APPLICATION NUMBER: US/10/416,708A

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Patentin version 3.2

SEQ ID NO 73

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Construct

US-10-416-708A-73

Query Match 98.9%; Score 1330; DB 6; Length 286;

Best Local Similarity 98.9%; Pred. No. 1.7e-119;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQOLGARVGYIELDNSGELLESFRSEERFPMMSTFKVLLCGAVLSRID 60
Db HPELVKVDADQOLGARVGYIELDNSGELLESFRSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 120
Db AGOEOLGRRIHYSQNDIVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGP 143
QY 121 KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGEILLTASRQ 180
Db KELTAFIHNMGDHYTRLDRWEPBELNEAIPNDRDITTPVAMATTIRKLLTGEILLTASRQ 203
QY 144 QLIDWMEADKVAQPLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTG 240
Db QLIDWMEADKVAQPLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNQIAEIGASLIKHW 263
Db SQATMDERNQIAEIGASLIKHW 286

RESULT 4

US-10-045-674A-523

Sequence 523, Application US/10045674A

GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: MASRI, HORACIO G.
APPLICANT: ROOKE, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DYAX/002 CIP2
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US/10/045,674A
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674A-523

Query Match 98.9%; Score 1330; DB 6; Length 286;
Best Local Similarity 98.9%; Pred. No. 1,7e-119;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDGLARVGYIELDINSGEILSPFSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQDGLARVGYIELDINSGEILSPFSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEQUGRIHYSQNDLVSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGGEQUGRIHYSQNDLVSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143
QY 121 KETLAFIHNMGDVTLDMEPELNEAIPNDESDTTTPVAMATTLRKLTGELLTASRQ 180
DB 144 KETLAFIHNMGDVTLDMEPELNEAIPNDESDTTTPVAMATTLRKLTGELLTASRQ 203
QY 181 QLTIDWMEADKVAQPLLRSAIPAGWFTADKSGAGERSGRIIALGPDGKRSRIIVITYTG 240
DB 204 QLTIDWMEADKVAQPLLRSAIPAGWFTADKSGAGERSGRIIALGPDGKRSRIIVITYTG 263
QY 241 SQATMDERNRQIAETIGASLIKHW 263
DB 264 SQATMDERNRQIAETIGASLIKHW 286

RESULT 5

US-09-490-324-285
Sequence 285, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Knappik, Achim

Ilag, Peter

Ge, Laming

Moroney, Simon

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490.324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 285:
US-09-490-324-285

Query Match 98.9%; Score 1330; DB 5; Length 299;
Best Local Similarity 98.9%; Pred. No. 1,9e-119;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDGLARVGYIELDINSGEILSPFSEERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQDGLARVGYIELDINSGEILSPFSEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGGEQUGRIHYSQNDLVSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 120
DB 84 AGGEQUGRIHYSQNDLVSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTTGGP 143
QY 121 KETLAFIHNMGDVTLDMEPELNEAIPNDESDTTTPVAMATTLRKLTGELLTASRQ 180
DB 144 KETLAFIHNMGDVTLDMEPELNEAIPNDESDTTTPVAMATTLRKLTGELLTASRQ 203
QY 181 QLTIDWMEADKVAQPLLRSAIPAGWFTADKSGAGERSGRIIALGPDGKRSRIIVITYTG 240
DB 204 QLTIDWMEADKVAQPLLRSAIPAGWFTADKSGAGERSGRIIALGPDGKRSRIIVITYTG 263
QY 241 SQATMDERNRQIAETIGASLIKHW 263
DB 264 SQATMDERNRQIAETIGASLIKHW 286

RESULT 6

US-09-490-324-298
Sequence 298, Application US/09490324

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Knappik, Achim

Ilag, Peter

Ge, Laming

Moroney, Simon

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 298:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 298:
US-09-490-324-298

Query Match 98.9%; Score 1330; DB 5; Length 299;
Best Local Similarity 98.9%; Pred. No. 1.9e-119;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	HPETLVKTKDAEDQGVAGVYIELDINSGETLESFRSEPRPMMSTFYLLCGAVLSRID	60
DB	24	HPETLVKTKDAEDQGVAGVYIELDINSGETLESFRSEPRPMMSTFYLLCGAVLSRID	83
QY	61	AGQELGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATIMSDNTAAILLTTIGSP	120
DB	84	AGQELGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATIMSDNTAAILLTTIGSP	143
QY	121	KELTAFLHMGDHYRLDRMEPELNEALPNDERDTTVPVAAATTLRKLLTGELTLASRQ	180
DB	144	KELTAFLHMGDHYRLDRMEPELNEALPNDERDTTVPVAAATTLRKLLTGELTLASRQ	203
QY	181	QLIDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSGIITAAIGPDGKPSRIVIYTTG	240
DB	204	QLIDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSGIITAAIGPDGKPSRIVIYTTG	263
QY	241	SOATMDERNROIAEIGASLIKHM	263
DB	264	SOATMDERNROIAEIGASLIKHM	286

RESULT 7
US-10-842-534-9
Sequence 300, Application US/09490324
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ge, Jaming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 300:
US-09-490-324-300

Query Match 98.9%; Score 1330; DB 5; Length 299;
Best Local Similarity 98.9%; Pred. No. 1.9e-119;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	HPETLVKTKDAEDQGVAGVYIELDINSGETLESFRSEPRPMMSTFYLLCGAVLSRID	60
DB	24	HPETLVKTKDAEDQGVAGVYIELDINSGETLESFRSEPRPMMSTFYLLCGAVLSRID	83
QY	61	AGQELGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATIMSDNTAAILLTTIGSP	120
DB	84	AGQELGRRIHSQNDLVEYSPVTEKHLTDGWTVELCSAATIMSDNTAAILLTTIGSP	143
QY	121	KELTAFLHMGDHYRLDRMEPELNEALPNDERDTTVPVAAATTLRKLLTGELTLASRQ	180
DB	144	KELTAFLHMGDHYRLDRMEPELNEALPNDERDTTVPVAAATTLRKLLTGELTLASRQ	203
QY	181	QLIDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSGIITAAIGPDGKPSRIVIYTTG	240
DB	204	QLIDMWEADKVAGPLLRSAIPAGWFIADKSGAGERSGIITAAIGPDGKPSRIVIYTTG	263
QY	241	SOATMDERNROIAEIGASLIKHM	263
DB	264	SOATMDERNROIAEIGASLIKHM	286

RESULT 8
US-10-842-534-9
Sequence 9, Application US/10842534
GENERAL INFORMATION:
APPLICANT: Stewart, Francis
Zhang, YOUNG
APPLICANT: Buchholz, Frank
TITLE OF INVENTION: NOVEL DNA CLONING METHOD
FILE REFERENCE: 2923-618
CURRENT APPLICATION NUMBER: US/10/842,534
PRIOR FILING DATE: 2004-05-11
PRIOR APPLICATION NUMBER: US 10/231,013
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 09/555,510
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: PCT/EP 98/07945
PRIOR FILING DATE: 1998-12-07
PRIOR APPLICATION NUMBER: EP 97121462.2
PRIOR FILING DATE: 1997-12-05


```
/ PRIOR APPLICATION NUMBER: EP 98118756.0
/ PRIOR FILING DATE: 1998-10-05
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 9
/ LENGTH: 286
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (1)..(286)
/ OTHER INFORMATION: bla gene on plasmid pBAD24-RecET at 3493-4353
US-10-842-534-9
```

```
Query Match          98.8%; Score 1329; DB 6; Length 286;
Best Local Similarity 98.5%; Pred. No. 2.2e-119;
Matches 259; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 HPEITLVKVDADQAGARVGYIELDINSGLIESFRSEERFPMMSTFKVLLCGAVLSRID 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 24 HPEITLVKVDADQAGARVGYIELDINSGLIESFRSEERFPMMSTFKVLLCGAVLSRID 83

QY 61 AGGEOIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 84 AGGEOIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143

QY 121 KELTAFILNMGGDVTRLDRWPEPELNEAIPNDESDTTTPVAMATTIRKLLTGELLTLASRQ 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 KELTAFILNMGGDVTRLDRWPEPELNEAIPNDESDTTTPVAMATTIRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVPGLIRLSALPAGMFTADKSGAGERSRGIITAAIGPDGKRSRIIVVITYTG 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 204 QLIDWMEADKVPGLIRLSALPAGMFTADKSGAGERSRGIITAAIGPDGKRSRIIVVITYTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 264 SQATMDERNRQIAEIGASLIKHW 286
```

```
RESULT 9
US-10-668-035-57
/ Sequence 57, Application US/10668035
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Hlaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Chen, Ruoping
/ TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled
/ TITLE OF INVENTION: Orphan Receptors
/ FILE REFERENCE: Azen0047
/ CURRENT APPLICATION NUMBER: US/10/668,035
/ CURRENT FILING DATE: 2003-09-22
/ PRIOR APPLICATION NUMBER: 60/094,879
/ PRIOR FILING DATE: 1998-07-31
/ PRIOR APPLICATION NUMBER: 60/106,300
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 60/110,906
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 57
/ LENGTH: 1293
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-668-035-57
```

```
Query Match          98.8%; Score 1329; DB 6; Length 1293;
Best Local Similarity 98.5%; Pred. No. 1.8e-118;
Matches 259; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 HPEITLVKVDADQAGARVGYIELDINSGLIESFRSEERFPMMSTFKVLLCGAVLSRID 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 245 HPEITLVKVDADQAGARVGYIELDINSGLIESFRSEERFPMMSTFKVLLCGAVLSRID 304

QY 61 AGGEOIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 305 AGGEOIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 364

QY 121 KELTAFILNMGGDVTRLDRWPEPELNEAIPNDESDTTTPVAMATTIRKLLTGELLTLASRQ 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 365 KELTAFILNMGGDVTRLDRWPEPELNEAIPNDESDTTTPVAMATTIRKLLTGELLTLASRQ 424

QY 181 QLIDWMEADKVPGLIRLSALPAGMFTADKSGAGERSRGIITAAIGPDGKRSRIIVVITYTG 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 425 QLIDWMEADKVPGLIRLSALPAGMFTADKSGAGERSRGIITAAIGPDGKRSRIIVVITYTG 484

QY 241 SQATMDERNRQIAEIGASLIKHW 263
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 485 SQATMDERNRQIAEIGASLIKHW 507
```

```
RESULT 10
US-10-622-088-114
/ Sequence 114, Application US/10622088
/ GENERAL INFORMATION:
/ APPLICANT: Bennett, Robert P.
/ APPLICANT: Welch, Peter J.
/ APPLICANT: Harwood, Steven
/ APPLICANT: Madden, Knut
/ APPLICANT: Primpson, Kenneth
/ APPLICANT: Franke, Kenneth E.
/ TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
/ FILE REFERENCE: 0942.5450007
/ CURRENT APPLICATION NUMBER: US/10/622,088
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: PCT/US03/22437
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: US 60/396,335
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: US 60/398,617
/ PRIOR FILING DATE: 2002-07-26
/ PRIOR APPLICATION NUMBER: US 60/427,231
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: US 60/456,496
/ PRIOR FILING DATE: 2003-03-24
/ PRIOR APPLICATION NUMBER: US 60/474,940
/ PRIOR FILING DATE: 2003-06-03
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 114
/ LENGTH: 265
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Amino acid sequence of a polypeptide having beta-lactamase activity
US-10-622-088-114
```

```
Query Match          98.0%; Score 1318; DB 6; Length 265;
Best Local Similarity 98.1%; Pred. No. 2.2e-116;
Matches 258; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 HPEITLVKVDADQAGARVGYIELDINSGLIESFRSEERFPMMSTFKVLLCGAVLSRID 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 HPEITLVKVDADQAGARVGYIELDINSGLIESFRSEERFPMMSTFKVLLCGAVLSRID 62

QY 61 AGGEOIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 AGGEOIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 122

QY 121 KELTAFILNMGGDVTRLDRWPEPELNEAIPNDESDTTTPVAMATTIRKLLTGELLTLASRQ 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 KELTAFILNMGGDVTRLDRWPEPELNEAIPNDESDTTTPVAMATTIRKLLTGELLTLASRQ 182
```

```
QY 181 QLDWMADKVAAGPLLSALPAGWFIADKSGAGERSGIIAIGPDGKSRIIVITTTG 240
DB 183 QLDWMADKVAAGPLLSALPAGWFIADKSGAGERSGIIAIGPDGKSRIIVITTTG 242
QY 241 SQATMDERNROIATIGASLIKHW 263
DB 243 SQATMDERNROIATIGASLIKHW 265

RESULT 11
US-10-491-653-146
; Sequence 146, Application US/10491653
; GENERAL INFORMATION:
; APPLICANT: Breitling, Frank
; APPLICANT: Moidebauer, Gerhard
; APPLICANT: Poustka, Annemarie
; APPLICANT: Kuhlwein, Thorsten
; APPLICANT: Luttgau, Sandra
; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins
; TITLE OF INVENTION: From said Libraries
; FILE REFERENCE: 4121-162
; CURRENT APPLICATION NUMBER: US/10/491,653
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: EP 01123596.7
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP02/10852
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 146
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-491-653-146

Query Match 96.8%; Score 1302; DB 6; Length 498;
Best Local Similarity 98.5%; Pred. No. 1.8e-116;
Matches 257; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 ETLVVKADPOLGARVGIYELDLSNGELLESFRSEERFPMMSTPKVLLCGAVLSRIDAG 62
DB 238 ETLVVKADPOLGARVGIYELDLSNGELLESFRSEERFPMMSTPKVLLCGAVLSRIDAG 297
QY 63 QEOLGRRIHYSNDIVESYPTVEKHLTDGMTVRELCSAITMSDNTANLLITTTGPKKE 122
DB 298 QEOLGRRIHYSNDIVESYPTVEKHLTDGMTVRELCSAITMSDNTANLLITTTGPKKE 357
QY 123 LTAFLHNGDHYTRLDRPEPELNEAIPNDERPTTPVMAATTLRKLLGELLTLASRQOL 182
DB 358 LTAFLHNGDHYTRLDRPEPELNEAIPNDERPTTPVMAATTLRKLLGELLTLASRQOL 417
QY 183 IDWMEADKVAAGPLLSALPAGWFIADKSGAGERSGIIAIGPDGKSRIIVITTTGSO 242
DB 418 IDWMEADKVAAGPLLSALPAGWFIADKSGAGERSGIIAIGPDGKSRIIVITTTGSO 477
QY 243 ATMDERNROIATIGASLIKHW 263
DB 478 ATMDERNROIATIGASLIKHW 498

RESULT 12
US-10-724-972A-6154
; Sequence 6154, Application US/10724972A
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Busi, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PAT03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
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; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 6154
; LENGTH: 306
; TYPE: PRT
; ORGANISM: S.epidermidis
US-10-724-972A-6154

Query Match 25.5%; Score 343.5; DB 6; Length 306;
Best Local Similarity 31.6%; Pred. No. 5.3e-25;
Matches 81; Conservative 62; Mismatches 108; Indels 5; Gaps 4;

QY 7 KVMDADPOLGARVGIYELDLSNGELLESFRSEERFPMMSTPKVLLCGAVLSRIDAGDOL 66
DB 51 ELNMLEKRYANIGVYALDITSGKEVK-FNADKFPAYASTSKAINSATLLGQV--YKTL 107
QY 67 GRRIHYSNDIVESYPTVEKHLTDGMTVRELCSAITMSDNTANLLITTTGPKELTAF 126
DB 108 NKVHINKDDIVASYPLEIKYVGDITLKELEASMKYSDNTANNKILNEIGGIKKIKR 167
QY 127 LHMNDHYTRLDRPEPELNEAIPNDERPTTPVMAATTLRKLLGELLTLASRQOLIDMM 186
DB 168 LKKLGDKVTNPRVELEINLYSPKSKDSTPAAFGKTLINKLIANGKSKKNKFLIDM 227
QY 187 EADKVAAGPLLSALPAGWFIADKSG-AGERSGIIAIGPDGKSRIIVITTTGSOATM 245
DB 228 LNNKNGDTLIDGVPKDKVADKSGQAITTASRNDVAIVYKNGSEPIIVITFTKONKS 287
QY 246 DERN-ROIATIGASLI 260
DB 288 DKPNDKLISETAKNVI 303

RESULT 13
US-10-414-532-65
; Sequence 65, Application US/10414532
; GENERAL INFORMATION:
; APPLICANT: CURTIS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 65
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: Sequence of blaSS-pspA-EFs668-bla C-term region in
; OTHER INFORMATION: pYA3637
US-10-414-532-65

Query Match 13.0%; Score 175; DB 6; Length 290;
Best Local Similarity 24.1%; Pred. No. 6.7e-09;
Matches 76; Conservative 38; Mismatches 101; Indels 100; Gaps 10;

QY 1 HETITVKVADADOLGA--RVGYIELDLSNGELLESFRSEERFPMMSTPKVLLCGAVLSR 58
DB 24 HETITVKVADAEELFQASNESQREADKTKIATQ--KDEBAAPATITRTIIVVEPSE 81
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